

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 03:05:25 ; Search time 1130 Seconds
(without alignments)
8759.686 Million cell updates/sec

Title: US-10-771-417-6

Perfect score: 1197

Sequence: 1 atgcacacgtggctacgtc.....aggacaagccctctctga 1197

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1197	100.0	1197	5	US-10-225-567A-476
2	1197	100.0	1197	6	US-10-295-027-747
3	1197	100.0	1197	6	US-10-295-027-822
4	1197	100.0	1197	8	US-10-771-417-6
5	1197	100.0	1197	9	US-10-847-918-9
6	1197	100.0	1450	8	US-10-833-829-1
7	1195.4	99.9	1197	3	US-09-796-338A-18
8	1195.4	99.9	1197	3	US-09-897-201-1
9	1195.4	99.9	1197	5	US-10-188-425-1
10	1195.4	99.9	1197	5	US-10-282-837-18
11	1195.4	99.9	1197	6	US-10-145-586-18
12	1195.4	99.9	1197	6	US-10-407-079-94
13	1195.4	99.9	1609	3	US-09-796-338A-16
14	1195.4	98.9	1609	5	US-10-282-837-16
15	1195.4	99.9	1609	6	US-10-145-586-16
16	1195.4	99.9	1609	6	US-10-407-079-92
17	1195.4	99.9	1609	8	US-10-757-262-31
18	1195.4	99.9	1617	6	US-10-241-220-48
19	1195.4	99.9	1617	8	US-10-872-972-48
20	1195.4	98.9	1617	8	US-10-872-991-48
21	1194.6	99.8	1197	9	US-10-451-002-1
22	1194.6	99.8	1197	9	US-10-451-002-3
23	1193.8	99.7	1197	8	US-10-782-021-1

24	1192.2	99.6	1197	8	US-10-149-826-45	Sequence 45, Appli
25	836.4	69.9	1191	3	US-09-930-910-1	Sequence 1, Appli
26	836.4	69.9	1191	8	US-10-771-417-2	Sequence 2, Appli
27	836.4	69.9	1237	3	US-09-897-201-3	Sequence 3, Appli
28	836.4	69.9	1237	5	US-10-188-425-3	Sequence 3, Appli
29	832	69.5	1188	9	US-10-240-224B-25	Sequence 25, Appli
30	832	69.5	1191	8	US-10-782-021-3	Sequence 3, Appli
31	832	69.5	1191	9	US-10-451-002-5	Sequence 5, Appli
32	832	69.5	1191	9	US-10-451-002-7	Sequence 7, Appli
33	808.8	67.6	1188	8	US-10-782-021-2	Sequence 2, Appli
34	600	50.1	600	10	US-11-060-756-4245	Sequence 4245, Ap
35	600	50.1	600	10	US-11-060-756-8517	Sequence 8517, Ap
36	245	20.5	548	3	US-09-801-944B-48	Sequence 48, Appli
37	187.8	15.7	1219	6	US-10-359-285-3	Sequence 3, Appli
38	186.8	15.6	1309	5	US-10-225-567A-365	Sequence 365, App
39	186.8	15.6	1365	2	US-08-899-112-29	Sequence 29, Appli
40	186.8	15.6	1365	6	US-10-298-992-4	Sequence 4, Appli
41	186.8	15.6	1365	6	US-10-285-019-27	Sequence 27, Appli
42	186.2	15.6	1164	5	US-10-228-264-3	Sequence 3, Appli
43	184.6	15.4	1164	3	US-09-826-509-504	Sequence 504, App
44	184.6	15.4	1164	8	US-10-925-095-504	Sequence 504, App
45	175	14.6	1257	3	US-09-943-007A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-225-567A-476

; Sequence 476, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: Lifespan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 476

; LENGTH: 1197

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-476

Query Match	100.0%	Score 1197;	DB 5;	Length 1197;
Best Local Similarity	100.0%;	Pred. No. 3e-246;		
Matches 1197;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCACACCGTGGCTACGTCGCGACCCCAACCGCTCTCGGGGGGCAACCGGCAACCGCTCC	60	
Db	1	ATGCACACCGTGGCTACGTCGCGACCCCAACCGCTCTCGGGGGGCAACCGGCAACCGCTCC	60	
QY	61	GGCTGCCCGGGCTGTGGGGCCCAACGCTTCGACGGCCAGTCCCTTCGCGGGGGCGGTG	120	
Db	61	GGCTGCCCGGGCTGTGGGGCCCAACGCTTCGACGGCCAGTCCCTTCGCGGGGGCGGTG	120	
QY	121	GACCGCTGGCTCGTGGCGGCTCTCTTCGCGGGCTGATGCTGGGGCTGTGGGGGAAC	180	
Db	121	GACCGCTGGCTCGTGGCGGCTCTCTTCGCGGGCTGATGCTGGGGCTGTGGGGGAAC	180	
QY	181	TCGCTGGTTCATCTACGTCACTGCGCGCAACGCGATGCGGACCGTGCACCACTTCTAC	240	
Db	181	TCGCTGGTTCATCTACGTCACTGCGCGCAACGCGATGCGGACCGTGCACCACTTCTAC	240	
QY	241	ATCGCCAACTGGGGGCCACGAGTGACCTTCCTCTGTGCTGGTCCCTTACGGCC	300	
Db	241	ATCGCCAACTGGGGGCCACGAGTGACCTTCCTCTGTGCTGGTCCCTTACGGCC	300	

Qy	301	CTGCTGATCACCGCTGCCCGCTGGGTGCTGGCGCACTTCATGTGCAAGTTGTTCAACTAC	360
Db	301	CTGCTGTACCGCTGCCCGCTGGGTGCTGGCGCACTTCATGTGCAAGTTGTTCAACTAC	360
Qy	361	ATCCAGCAGGTCTCGGTGCAAGCCACGTGTGCCACTCTGTGACCGCCATGAGTGTGGACGC	420
Db	361	ATCCAGCAGGTCTCGGTGCAAGCCACGTGTGCCACTCTGTGACCGCCATGAGTGTGGACGC	420
Qy	421	TGTTACGTGACGGTTCCTCGTTGGCGGCCTGTACCGCGCACGCCCCGCCCTGGCGCTG	480
Db	421	TGTTACGTGACGGTTCCTCGTTGGCGGCCTGTACCGCGCACGCCCCGCCCTGGCGCTG	480
Qy	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTCGCGCGGTGTCTGCGCGCGTGTCTGCCCTG	540
Db	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGCGGTGTCTGCGCGCGTGTCTGCCCTG	540
Qy	541	CACCGCTGTCAACCGGCGCGCGCTACTGTGAGTGAGGCCCTTCCCGACGCGCGCTG	600
Db	541	CACCGCTGTCAACCGGCGCGCGCTACTGTGAGTGAGGCCCTTCCCGACGCGCGCTG	600
Qy	601	GAGCGCGCTTCGCACTGTACAACTGCTGGCGTGTACCTGTGCTGCCGTGCTGCCAC	660
Db	601	GAGCGCGCTTCGCACTGTACAACTGCTGGCGTGTACCTGTGCTGCCGTGCTGCCAC	660
Qy	661	TGCGCTGTCTATGCGGCATGCTCGGCACCTGCGCGCGGTGCGCGTGTGCGCGCGCG	720
Db	661	TGCGCTGTCTATGCGGCATGCTCGGCACCTGCGCGCGGTGCGCGTGTGCGCGCGCG	720
Qy	721	GCGGATAGCGCTTGCAGGGGCAAGTGTGTGCAGAGCGCGCAGCGCGTGTGCGGCGCAAG	780
Db	721	GCGGATAGCGCTTGCAGGGGCAAGTGTGTGCAGAGCGCGCAGCGCGTGTGCGGCGCAAG	780
Qy	781	GTCTCGCGGTGTGTGGCGCGTGGTCTGTCTTGTGCGCGCTGTGTGGCGCGCGCGCG	840
Db	781	GTCTCGCGGTGTGTGGCGCGTGGTCTGTCTTGTGCGCGCTGTGTGGCGCGCGCGCG	840
Qy	841	CTGTTCTGTGTGTGTCAGGGCTGGGCGCGCGGCTCTTGGCACCCAGCAGCAGCTAGCG	900
Db	841	CTGTTCTGTGTGTGTCAGGGCTGGGCGCGCGGCTCTTGGCACCCAGCAGCAGCTAGCG	900
Qy	901	GCCTACGCGCTTAAGACTGCGGTCTACTGTGATGCTTACAGCAACTCCGCGCTGAACCG	960
Db	901	GCCTACGCGCTTAAGACTGCGGTCTACTGTGATGCTTACAGCAACTCCGCGCTGAACCG	960
Qy	961	CTGCTCTACGCTTCTGTGGGTCCGACTTCCGACAGAGCTTCCGCGCGGTGTGCCCTGC	1020
Db	961	CTGCTCTACGCTTCTGTGGGTCCGACTTCCGACAGAGCTTCCGCGCGGTGTGCCCTGC	1020
Qy	1021	GCG	1080
Db	1021	GCG	1080
Qy	1081	GCGGAGCTGCACCGCTGGGTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1140
Db	1081	GCGGAGCTGCACCGCTGGGTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1140
Qy	1141	AGTGGGTGCGCGCGCGCGCTGTGGTCTGTGGGAGAGCAACCGCCCTCTCTGA	1197
Db	1141	AGTGGGTGCGCGCGCGCGCTGTGGTCTGTGGGAGAGCAACCGCCCTCTCTGA	1197

RESULT 2

US-10-295-027-747
; Sequence 747, Application US/10295027
; Publication No. US200323350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Ariz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynnne, Richard
; APPLICANT: Hevesi, Peter A.

Qy	1081	GCAGAGCTGCACCGCTGTGGGTCCACCGGCCCCCGCAGAGCGGCAGAGCCAGGGAGC	1140
Db	1081	CGGAGCTGCACCGCTGTGGGTCCACCGGCCCCCGCAGAGCGGCAGAGCCAGGGAGC	1140
Qy	1141	AGTGGGCTGACCGCGCGCGGCTGTGGTCTCTGGGGGAGGACAAACGCCCTCTCTGA	1197
Db	1141	AGTGGGCTGACCGCGCGCGGCTGTGGTCTCTGGGGGAGGACAAACGCCCTCTCTGA	1197

RESULT 5

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US-10-847-918-9
; Sequence 9, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-9

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Query Match	100.0%;	Score 1197;	DB 9;	Length 1197;
Best Local Similarity	100.0%;	Pred. No. 3e-246;		
Matches 1197;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	ATGCACACCGTGGCTACGTCGGACCCAAACGCGTCTCTGGGGGGACACGGCCAAACGCTCC	60
Db	1	ATGCACACCGTGGCTACGTCGGACCCAAACGCGTCTCTGGGGGGACACGGCCAAACGCTCC	60
Qy	61	GGCTGCCCGGGCTGTGGGGCCAAACGCTCTGGACGGCCAGTCCCTTTCGCCCGGGGGCGTG	120
Db	61	GGCTGCCCGGGCTGTGGGGCCAAACGCTCTGGACGGCCAGTCCCTTTCGCCCGGGGGCGTG	120
Qy	121	GAGCCTTGGCTGTGGCCGCTCTTCTTTCGGCGCGTGTGCTGTGGGCTCGTGGGGGAAC	180
Db	121	GAGCCTTGGCTGTGGCCGCTCTTCTTTCGGCGCGTGTGCTGTGGGCTCGTGGGGGAAC	180
Qy	181	TCGCTGTGTATCTACGTATCTGCCGCCACAAGCCGATGCGGACCGTGACCAACTTCTAC	240
Db	181	TCGCTGTGTATCTACGTATCTGCCGCCACAAGCCGATGCGGACCGTGACCAACTTCTAC	240
Qy	241	ATCGCCAACTTGGGGCCACGGACGTGACTTCTCTGTGTGCTGCTGCTCCCTTCAAGGCC	300
Db	241	ATCGCCAACTTGGGGCCACGGACGTGACTTCTCTGTGTGCTGCTGCTCCCTTCAAGGCC	300
Qy	301	CTGCTGTACCGCTGCCCGGCTGGTGTCTGGCGACTTCATGTGCAGTTGCTCAACTAC	360
Db	301	CTGCTGTACCGCTGCCCGGCTGGTGTCTGGCGACTTCATGTGCAGTTGCTCAACTAC	360
Qy	361	ATCCAGCAGGTCTCGGTGACGGCCACGTTGCCACTCTGACCGCCATGAGTGTGGACCGC	420
Db	361	ATCCAGCAGGTCTCGGTGACGGCCACGTTGCCACTCTGACCGCCATGAGTGTGGACCGC	420
Qy	421	TGTTACGTGACGGTGTCTCCGTTTGGCGGCCCTTGACCGCCACGGCCCCGGCTGGCGGTG	480
Db	421	TGTTACGTGACGGTGTCTCCGTTTGGCGGCCCTTGACCGCCACGGCCCCGGCTGGCGGTG	480
Qy	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTCTGGGGGGTGTCTGGCCGGTGTCTGCCGCTG	540
Db	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTCTGGGGGGTGTCTGGCCGGTGTCTGCCGCTG	540

PRECIT.T. 6

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US-10-833-829-1
; Sequence 1, Application US/10833829
; Publication No. US20050026224A1
; GENERAL INFORMATION:
; APPLICANT: Follettie, Maximillian T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR 54
; FILE REFERENCE: 102729-20
; CURRENT APPLICATION NUMBER: US/10/833,829
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: 60/466,132
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1197)
US-10-833-829-1

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Query Match 100.0%; Score 1197; DB 8; Length 1450;
Best Local Similarity 100.0%; Pred. No. 2.9e-246;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICANT: Follett, Maximilian T.

QY 1 ATGCACCGCTGGCTACGTCGGACCCAAACGGTCTCTGGGGGACACGGCCAAACGCTCC 60
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1 ATGCACACCGTGGCTACGTCGGACCCAAACGGTCTCTGGGGGACACGGCCAAACGCTCC 60
QY 61 GGTCTCCCGGGCTGTGGGCGCAAAACGCTCGAGAGCGCCAGTCCCTTCGCCCGCGGCGGTG 120
Db |||||
61 GGTCTCCCGGGCTGTGGGCGCAAAACGCTCGAGAGCGCCAGTCCCTTCGCCCGCGGCGGTG 120
QY 121 GACGCTCGGCTGTGGCGGCTCTCTTCCTCGCGGCGCTGATGCTGCTGGGCTCTGGTGGGAAC 180
Db |||||
121 GACGCTCGGCTGTGGCGGCTCTCTTCCTCGCGGCGCTGATGCTGCTGGGCTCTGGTGGGAAC 180
QY 181 TCGCTGTGTCATCTAGTCTATCTGCGCGCACAGCCGATGCGGACCGTGAACACTTCTAC 240
Db |||||
181 TCGCTGTGTCATCTAGTCTATCTGCGCGCACAGCCGATGCGGACCGTGAACACTTCTAC 240
QY 241 ATCGCCAACTGGCGGCGCACGAGCTACCTTCCTGCTGTGCTGGTCCCTTCACGGCC 300
Db |||||
241 ATCGCCAACTGGCGGCGCACGAGCTACCTTCCTGCTGTGCTGGTCCCTTCACGGCC 300
QY 301 CTGCTGTACCGCTGCGCGCTGGGTGTGGGCGACTTTCATGTGCAAGTTCGTCAACTAC 360
Db |||||
301 CTGCTGTACCGCTGCGCGCTGGGTGTGGGCGACTTTCATGTGCAAGTTCGTCAACTAC 360
QY 361 ATCCAGCAGGCTCGGTGACGGCCACGCTGTGCCACTCTGACGGCCATGAGTGTGGACCGC 420
Db |||||
361 ATCCAGCAGGCTCGGTGACGGCCACGCTGTGCCACTCTGACGGCCATGAGTGTGGACCGC 420
QY 421 TGGTACGTCAGGCTGTCCGTTGGCGGCTTCCGCGGCTTCGCGCGGCTCTGCCCTTCG 480
Db |||||
421 TGGTACGTCAGGCTGTCCGTTGGCGGCTTCCGCGGCTTCGCGCGGCTCTGCCCTTCG 480
QY 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGGCGGGTGTCTGCGCGGCTCTGCCCTTCG 540
Db |||||
481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGGCGGGTGTCTGCGCGGCTCTGCCCTTCG 540
QY 541 CACCGCTGTACCGCGGCGCGGCTTACTGCACTGAGGCTTCCTCCAGCGCGGCGCTG 600
Db |||||
541 CACCGCTGTACCGCGGCGCGGCTTACTGCACTGAGGCTTCCTCCAGCGCGGCGCTG 600
QY 601 GAGCGCGCTTCGCACTGCAAACTGCTGGCGCTGTACTCTGCTGCTGCTGCTGCTGCTGCTG 660
Db |||||
601 GAGCGCGCTTCGCACTGCAAACTGCTGGCGCTGTACTCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 TCGCGCTGTATGCGGCGATGTCGCGCACTGTGGGCGGGTGTGCGTGTGCGGCGGCGCC 720
Db |||||
661 TCGCGCTGTATGCGGCGATGTCGCGCACTGTGGGCGGGTGTGCGTGTGCGGCGGCGCC 720
QY 721 GCGGATAGCGGCTGACGGGCGAGTGTGGCAGAGCGGCGGCGGCGGCGGCGGCGGCGG 780
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721 GCGGATAGCGGCTGACGGGCGAGTGTGGCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
QY 781 GTCTCGCGCTGTGGCGGCGTGTCTGCTCTTTCGCGGCTGTGCTGGGCGGCGGCGGCGG 840
Db |||||
781 GTCTCGCGCTGTGGCGGCGTGTCTGCTCTTTCGCGGCTGTGCTGGGCGGCGGCGGCGG 840
QY 841 CTGTTCTGTGTGCTGACGGCGTGGGCGGCGGCGGCTCTGCGACCCACGAGCTAGCGCC 900
Db |||||
841 CTGTTCTGTGTGCTGACGGCGTGGGCGGCGGCGGCTCTGCGACCCACGAGCTAGCGCC 900
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Db |||||
901 GCCTACGCGCTTAAGACTTGGGCTCACTGTCATGTCTTACAGCACTCGCGCTGAACCCG 960
QY 961 CTGCTCTACGCTTCTCTGGGCTCGCACTTCGACAGGCTTCGCGCGGCTCTGCCCTTCG 1020
Db |||||
961 CTGCTCTACGCTTCTCTGGGCTCGCACTTCGACAGGCTTCGCGCGGCTCTGCCCTTCG 1020
QY 1021 GCG 1080
Db |||||
1021 GCG 1080
QY 1081 GCGGAGCTGCACCGGCTGGGGTCCACCCGGGCGGCGGCGGCGGCGGCGGCGGCGG 1140

Db 1081 GCGGAGCTGCACCGGCTGGGGTCCACCCGGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
QY 1141 AGTGGGCTGGCGCGCGCGGCGTGTGCGTCTGTTGGGGAGGACAAACGCGCTCTCTGA 1197
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1141 AGTGGGCTGGCGCGCGCGGCGTGTGCGTCTGTTGGGGAGGACAAACGCGCTCTCTGA 1197
RESULT 7
US-09-796-338A-18
; Sequence 18, Application US/09796338A
; Patent No. US20020061522A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/09/796,338A
; CURRENT FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-338A-18
Query Match 99.9%; Score 1195.4; DB 3; Length 1197;
Best Local Similarity 99.9%; Pred. No. 6.6e-246;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCACACCGTGGCTACGTCGGACCCAAACGGTCTCTGGGGGACACGGCCAAACGCTCC 60
Db 1 ATGCACACCGTGGCTACGTCGGGCGCCAAACGGTCTCTGGGGGACACGGCCAAACGCTCC 60
QY 61 GGTCTCCCGGGCTGTGGGCGCAACGCTCGGACGGCCAGTCCCTTCGCCCGCGGCGGTG 120
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QY 721 GCCGATAGCGCGCTTCGAGGGGAGGTGTGCGCAGAGCGCGCAGGGCGCGCTGCGGGCAAG 780
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QY 841 CTGTTCTCTGCTGCGCGCATGTGCGCGCGCGCGCGCGCTGCGCGCGCATTCAC 900
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QY 901 GCTACGCGCTTAAGACCTTGGGCTCACTGCACTGTCTACAGCAACTCCGCGCTGAACCG 960
Db |||||
QY 901 GCTACGCGCTTAAGACCTTGGGCTCACTGCACTGTCTACAGCAACTCCGCGCTGAACCG 960
Db |||||
QY 961 CTGCTCTACGCTTCTGCGCTGCGCACTTCGACAGGCTTCGCGCGCTGCGCGCTG 1020
Db |||||
QY 961 CTGCTCTACGCTTCTGCGCTGCGCACTTCGACAGGCTTCGCGCGCTGCGCGCTG 1020
Db |||||
QY 1021 GCG 1080
Db |||||
QY 1021 GCG 1080
Db |||||
QY 1081 GCGGAGCTGCAACGCTTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db |||||
QY 1081 GCGGAGCTGCAACGCTTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db |||||
QY 1141 AGTGGCTGGCGCGCGCGCGCGCTGTGCTGCTGCTGGGGAGGACAAAGCCCTCTCTGA 1197
Db |||||
QY 1141 AGTGGCTGGCGCGCGCGCGCGCTGTGCTGCTGCTGGGGAGGACAAAGCCCTCTCTGA 1197
Db |||||

RESULT 8
US-09-897-201-1
; Sequence 1, Application US/09897201
; Patent No. US20020077469A1
; GENERAL INFORMATION:
; APPLICANT: BOROMSKI, BETH E
; APPLICANT: QUAN, YONG
; APPLICANT: SMITH, KELLI E
; TITLE OF INVENTION: DNA ENCODING ORPHAN SNORF 11 RECEPTOR
; FILE REFERENCE: 1795/58800a
; CURRENT APPLICATION NUMBER: US/09/897,201
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: 09/266,127
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-897-201-1

Query Match 99.9%; Score 1195.4; DB 3; Length 1197;
Best Local Similarity 99.9%; Pred.No. 6.6e-246;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCACACCGTGGCTACGTCCGGACCAACGGCTCTGCGGGGACCGCGCCAAAGCCCTCC 60
Db |||||
QY 1 ATGCACACCGTGGCTACGTCCGGACCAACGGCTCTGCGGGGACCGCGCCAAAGCCCTCC 60
Db |||||
QY 61 GGTCTCCCGGGTGTGGCGCCAAAGCTGCGAGCGCCCAAGTCCCTTCGCGCGCGCGCTG 120
Db |||||

Db 61 GGTCTCCCGGGTGTGGCGCCAAAGCTGCGAGCGCCCAAGTCCCTTCGCGCGCGCGCTG 120
QY 121 GAGCGCTGCGCTGCGCGCTCTTCTTTCGCGCGCTGTGCTGCTGCGCGCTGCTGCGCGAAC 180
Db |||||
QY 121 GAGCGCTGCGCTGCGCGCTCTTCTTTCGCGCGCTGTGCTGCTGCGCGCTGCTGCGCGAAC 180
Db |||||
QY 181 TCGCTGCTCATCTACGTTCATCTGCGCGCCAAAGCGAGTGGCGACCGTGAACAACTTCTAC 240
Db |||||
QY 181 TCGCTGCTCATCTACGTTCATCTGCGCGCCAAAGCGAGTGGCGACCGTGAACAACTTCTAC 240
Db |||||
QY 241 ATCGCCAACTGCGCGCGCCAAAGCGAGTGGCGACCGTGAACAACTTCTAC 300
Db |||||
QY 241 ATCGCCAACTGCGCGCGCCAAAGCGAGTGGCGACCGTGAACAACTTCTAC 300
Db |||||
QY 301 CTGCTGTACCGCTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 360
Db |||||
QY 301 CTGCTGTACCGCTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 360
Db |||||
QY 361 ATCCAGCAGGCTCTCGGTGCGCGCCAAAGCGAGTGGCGACCGTGAACAACTTCTAC 420
Db |||||
QY 361 ATCCAGCAGGCTCTCGGTGCGCGCCAAAGCGAGTGGCGACCGTGAACAACTTCTAC 420
Db |||||
QY 421 TGGTACGTGAGCGGTTCCTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 480
Db |||||
QY 421 TGGTACGTGAGCGGTTCCTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 480
Db |||||
QY 481 GCTGTACCGCTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 540
Db |||||
QY 481 GCTGTACCGCTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 540
Db |||||
QY 541 CACCGCTGTCAACCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 600
Db |||||
QY 541 CACCGCTGTCAACCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 600
Db |||||
QY 601 GAGCGCGCTTTCGCACTGTGTAACAACTGCGCGCTGCTGCTGCGCGCTGCTGCGCGAAC 660
Db |||||
QY 601 GAGCGCGCTTTCGCACTGTGTAACAACTGCGCGCTGCTGCTGCGCGCTGCTGCGCGAAC 660
Db |||||
QY 661 TCGCGCTGCTATGCGCGCATGTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 720
Db |||||
QY 661 TCGCGCTGCTATGCGCGCATGTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 720
Db |||||
QY 721 GCCGATAGCGCGCTTCGAGGGGAGGTGTGCGCAGAGCGCGCAGGGCGCGCTGCGGGCAAG 780
Db |||||
QY 721 GCCGATAGCGCGCTTCGAGGGGAGGTGTGCGCAGAGCGCGCAGGGCGCGCTGCGGGCAAG 780
Db |||||
QY 781 GTCTCGCGCTGTGCGCGCATGTGCTGCTCTTTCGCGCGCTGTGCGCGCGCATTCAC 840
Db |||||
QY 781 GTCTCGCGCTGTGCGCGCATGTGCTGCTCTTTCGCGCGCTGTGCGCGCGCATTCAC 840
Db |||||
QY 841 CTGTTCTCTGCTGCGCGCATGTGCGCGCGCGCGCGCGCTGCGCGCGCATTCAC 900
Db |||||
QY 841 CTGTTCTCTGCTGCGCGCATGTGCGCGCGCGCGCGCGCTGCGCGCGCATTCAC 900
Db |||||
QY 901 GCCTACGCGCTTAAGACCTTGGGCTCACTGCACTGTCTACAGCAACTCCGCGCTGAACCG 960
Db |||||
QY 901 GCCTACGCGCTTAAGACCTTGGGCTCACTGCACTGTCTACAGCAACTCCGCGCTGAACCG 960
Db |||||
QY 961 CTGCTCTACGCTTCTGCGCTGCGCACTTCGACAGGCTTCGCGCGCTGCGCGCTG 1020
Db |||||
QY 961 CTGCTCTACGCTTCTGCGCTGCGCACTTCGACAGGCTTCGCGCGCTGCGCGCTG 1020
Db |||||
QY 1021 GCG 1080
Db |||||
QY 1021 GCG 1080
Db |||||
QY 1081 GCGGAGCTGCAACGCTTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db |||||
QY 1081 GCGGAGCTGCAACGCTTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db |||||
QY 1141 AGTGGCTGGCGCGCGCGCGCTGTGCTGCTGCTGGGGAGGACAAAGCCCTCTCTGA 1197
Db |||||
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Db |||||


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RESULT 9
US-10-188-425-1
; Sequence 1, Application US/10188425
; Publication No. US20030022839A1
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; TITLE OF INVENTION: RECEPTOR AGONISTS USEFUL FOR THE TREATMENT OF PAIN
; FILE REFERENCE: 1795/58800-B
; CURRENT APPLICATION NUMBER: US/10/188,425
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 09/897,201
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: 09/266,127
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-188-425-1

Query Match      99.9%; Score 1195.4; DB 5; Length 1197;
Best Local Similarity 99.9%; Pred. No. 6.6e-246;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGCACACCGTGGCTACGTCGGACCCAAACCGTCCTGGGGGGCACCGGCCAAACGCTCC 60
DB      1  ATGCACACCGTGGCTACGTCGGACCCAAACCGTCCTGGGGGGCACCGGCCAAACGCTCC 60

QY      61  GGCTGCCCGGGCTGTGGCGCAACGCTTCGACAGCGCCAGTCCTTCGCGCGGGCGGTG 120
DB      61  GGCTGCCCGGGCTGTGGCGCAACGCTTCGACAGCGCCAGTCCTTCGCGCGGGCGGTG 120

QY      121  GACGCTGGCTGTGGCGGTCTTCTTTCGCGCGGTGATGCTGTGGGCGCTGTGGGGAAC 180
DB      121  GACGCTGGCTGTGGCGGTCTTCTTTCGCGCGGTGATGCTGTGGGCGCTGTGGGGAAC 180

QY      181  TCGTGTGGTCACTACGTATCTGCGCCACCAAGCCGATGCGGACCGTGACCACTTCTAC 240
DB      181  TCGTGTGGTCACTACGTATCTGCGCCACCAAGCCGATGCGGACCGTGACCACTTCTAC 240

QY      241  ATCGCCAACTGGCGGCCACGAGCGTACCTTCTCTGTGCTGCTGCTGCTTCCAGCGCC 300
DB      241  ATCGCCAACTGGCGGCCACGAGCGTACCTTCTCTGTGCTGCTGCTGCTTCCAGCGCC 300

QY      301  CTGCTGTACCGCTGCGCGGCTGGGTGCTGGGCGACTTCATGTGCAAGTTGCTCAACTAC 360
DB      301  CTGCTGTACCGCTGCGCGGCTGGGTGCTGGGCGACTTCATGTGCAAGTTGCTCAACTAC 360

QY      361  ATCCAGCAGGTCCTGGTGCAGGCCACAGTGTCCCACTGTACCGCCATGAGTGTGACCGC 420
DB      361  ATCCAGCAGGTCCTGGTGCAGGCCACAGTGTCCCACTGTACCGCCATGAGTGTGACCGC 420

QY      421  TGGTACGTGACGCGTGTCCCGCTTGGCGCCCTTGACCGCCGACCGCCCGCTGGCGGTG 480
DB      421  TGGTACGTGACGCGTGTCCCGCTTGGCGCCCTTGACCGCCGACCGCCCGCTGGCGGTG 480

QY      481  GCTGTACGCTCAGCATCTGGGTAGGCTCTCGGGGGGTGTCTGGCGGGGTGCTCGCCGTG 540
DB      481  GCTGTACGCTCAGCATCTGGGTAGGCTCTCGGGGGGTGTCTGGCGGGGTGCTCGCCGTG 540

QY      541  CACCGCTGTACCGGGCGCGGCTTACTGACGTAGGCTTCCCGACCGCGCGCGCTG 600
DB      541  CACCGCTGTACCGGGCGCGGCTTACTGACGTAGGCTTCCCGACCGCGCGCGCTG 600

QY      601  GAGCGCGCTTTCGCACTGTACAACTGCTGGCGGTGTACCTGTGCTGCTGCTGCTGCTG 660
DB      601  GAGCGCGCTTTCGCACTGTACAACTGCTGGCGGTGTACCTGTGCTGCTGCTGCTGCTG 660
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QY      661  TGGCCTGTATGGGCCATGCTGGCCACACTGGGCGGGGTGCGCGTGGCGCCCGCGCC 720
DB      661  TGGCCTGTATGGGCCATGCTGGCCACACTGGGCGGGGTGCGCGTGGCGCCCGCGCC 720

QY      721  GCGATAGCGCCCTTCAGAGGGCAGGTGCTGGCAGAGCGCGCAGGCGCGGTGCGGGCCAAAG 780
DB      721  GCGATAGCGCCCTTCAGAGGGCAGGTGCTGGCAGAGCGCGCGAGGCGCGGTGCGGGCCAAAG 780

QY      781  GTCTCGCGGTGTGGCGCGGTGGTCTCTCTTTCGCCGCTTCTGGGGCCCCCATCCAG 840
DB      781  GTCTCGCGGTGTGGCGCGGTGGTCTCTCTTTCGCCGCTTCTGGGGCCCCCATCCAG 840

QY      841  CTGTTCTGTGTGCTGAGGGCGCTGGGCGCGCGGGCTCTGGGACCCACGACGACTACGCC 900
DB      841  CTGTTCTGTGTGCTGAGGGCGCTGGGCGCGCGGGCTCTGGGACCCACGACGACTACGCC 900

QY      901  GCCTACGCGCTTAAGACCTGGGCTCACTGATGTCCTACAGCAACTCCGCGCTCAACCCG 960
DB      901  GCCTACGCGCTTAAGACCTGGGCTCACTGATGTCCTACAGCAACTCCGCGCTCAACCCG 960

QY      961  CTGCTTACGCTTCTTGGGCTCGCACTTCGACAGCGCTTCGCGCGGTGCTGCCCCCTGC 1020
DB      961  CTGCTTACGCTTCTTGGGCTCGCACTTCGACAGCGCTTCGCGCGGTGCTGCCCCCTGC 1020

QY      1021  GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
DB      1021  GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080

QY      1081  GCGGAGCTGCACCGCTTGGGTCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGC 1140
DB      1081  GCGGAGCTGCACCGCTTGGGTCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGC 1140

QY      1141  AGTGGGCTGCGCGCGCGCGGTGTGCTGTGGGGAGGACAAAGCGCCCTCTCTGA 1197
DB      1141  AGTGGGCTGCGCGCGCGGTGTGCTGTGGGGAGGACAAAGCGCCCTCTCTGA 1197

RESULT 10
US-10-282-837-18
; Sequence 18, Application US/10282837
; Publication No. US20030082738A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; FILE REFERENCE: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/10/282,837
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/796,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-837-18

Query Match      99.9%; Score 1195.4; DB 5; Length 1197;
Best Local Similarity 99.9%; Pred. No. 6.6e-246;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGCACACCGTGGCTACGTCGGACCCAAACCGTCCTGGGGGGCACCGGCCAAACGCTCC 60
DB      1  ATGCACACCGTGGCTACGTCGGACCCAAACCGTCCTGGGGGGCACCGGCCAAACGCTCC 60

QY      61  GGCTGCCCGGGCTGTGGCGCAACGCTTCGACAGCGCCAGTCCTTCGCGCGGGCGGTG 120
DB      61  GGCTGCCCGGGCTGTGGCGCAACGCTTCGACAGCGCCAGTCCTTCGCGCGGGCGGTG 120

QY      121  GACGCTGGCTGTGGCGGTCTTCTTTCGCGCGGTGATGCTGTGGGCGCTGTGGGGAAC 180
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121	Db	 GAGCGCTGCTCGTGGCGCTCTTCTTTCGGGGCGCTGATGCTGCTGGCGCTGGTGGGAGAC	180
181	Qy	 TCGCTGCTCATCTAGCTCATCTGCGGCCACAAGCGGATGCGGAGCGTGAGCAACATTTCTAC	240
181	Db	 TCGCTGGTTCATCTAGCTCATCTGCGGCCACAAGCGGATGCGGAGCGTGAGCAACATTTCTAC	240
241	Qy	 ATCGCAACCTTGGGGCCACGAGAGTGAACCTTCTCTGTGCTGCGTCCCTTTCACGGCC	300
241	Db	 ATCGCAACCTTGGGGCCACGAGAGTGAACCTTCTCTGTGCTGCGTCCCTTTCACGGCC	300
301	Qy	 CTGCTGTATCCCGCTGCCGGCTGGGTGCTGGGGCGACTTCATGTGCAAGTTGTTCAACTAC	360
301	Db	 CTGCTGTATCCCGCTGCCGGCTGGGTGCTGGGGCGACTTCATGTGCAAGTTGTTCAACTAC	360
361	Qy	 ATTCAGCAGAGTCTCGGTGCAAGCCACAGTGTGCCACTCTGACCGGCATGAGTGTGGACGC	420
361	Db	 ATTCAGCAGAGTCTCGGTGCAAGCCACAGTGTGCCACTCTGACCGGCATGAGTGTGGACGC	420
421	Qy	 TGGTACGTGACGGTGTCCCGTTGCGCGCTGACCGCGCTGACCGCGCCCGCTGGCGCGTG	480
421	Db	 TGGTACGTGACGGTGTCCCGTTGCGCGCTGACCGCGCTGACCGCGCCCGCTGGCGCGTG	480
481	Qy	 GCTGTACGCTTCAGCATCTGGTATAGGCTCTCGCGGGTGTCTGCGCGGTGCTCGCGCTG	540
481	Db	 GCTGTACGCTTCAGCATCTGGTATAGGCTCTCGCGGGTGTCTGCGCGGTGCTCGCGCTG	540
541	Qy	 CACCGCTGTACCCGGGCCCGCGCTACTGCTAGTGAGGCTTCCCGAGCGCGCGCTG	600
541	Db	 CACCGCTGTACCCGGGCCCGCGCTACTGCTAGTGAGGCTTCCCGAGCGCGCGCTG	600
601	Qy	 GAGCGCGCTTCGCACTGTACAACTGTGTGCGCTGTACTGTCTGCGCTGCTGCGCCACC	660
601	Db	 GAGCGCGCTTCGCACTGTACAACTGTGTGCGCTGTACTGTCTGCGCTGCTGCGCCACC	660
661	Qy	 TGGCGCTGTATGCGGCCATGCTGGGCAACTGTGGCCGGGTGCGCGTGGCCCCCGCGCC	720
661	Db	 TGGCGCTGTATGCGGCCATGCTGGGCAACTGTGGCCGGGTGCGCGTGGCCCCCGCGCC	720
721	Qy	 GCCGATAGCGCCCTGCAAGGGCAGGTGTGCGAGCGCGGAGCGCGCTGGGGGCCAAG	780
721	Db	 GCCGATAGCGCCCTGCAAGGGCAGGTGTGCGAGCGCGGAGCGCGCTGGGGGCCAAG	780
781	Qy	 GTCTCGCGGCTGTGGCGCGTGGTCTGTCTTTCGCGGCTGCTGGGGCCCCCATCCAG	840
781	Db	 GTCTCGCGGCTGTGGCGCGTGGTCTGTCTTTCGCGGCTGCTGGGGCCCCCATCCAG	840
841	Qy	 CTGTTCTGTGTGCTGAGGGCGCTGGGCCCGCGGGCTCTGGGACCAACGAGAGCTAGCC	900
841	Db	 CTGTTCTGTGTGCTGAGGGCGCTGGGCCCGCGGGCTCTGGGACCAACGAGAGCTAGCC	900
901	Qy	 GCCTACGCGCTTAAGACTGGGCTCACTGCAATGCTTACAGCACTCCGGCTGGAACCCG	960
901	Db	 GCCTACGCGCTTAAGACTGGGCTCACTGCAATGCTTACAGCACTCCGGCTGGAACCCG	960
961	Qy	 CTGCTTACGCTTCTCTGGGCTGCACCTTCGACAGGCTTTCGCGCGGCTGTGCCCTGC	1020
961	Db	 CTGCTTACGCTTCTCTGGGCTGCACCTTTCGACAGGCTTTCGCGCGGCTGTGCCCTGC	1020
1021	Qy	 GCGCGGCGCGCCCCCGCGCGCCCCCGCGGGCCGGAACCTGTGGACCCCGAGCCCCAC	1080
1021	Db	 GCGCGGCGCGCCCCCGCGCGCCCCCGCGGGCCGGAACCTGTGGACCCCGAGCCCCAC	1080
1081	Qy	 GCGGAGTGTACACGCTTGGGTGCCACCCCGCGCCCCCGAGGGCGGAGAGCCAGGGAGC	1140
1081	Db	 GCGGAGTGTACACGCTTGGGTGCCACCCCGCGCCCCCGAGGGCGGAGAGCCAGGGAGC	1140
1141	Qy	 AGTGGGCTGGCCGCGCGGCTGTGCTGTGGGGAGGAGCAACGCCCCCTCTCTGA	1197
1141	Db	 AGTGGGCTGGCCGCGCGGCTGTGCTGTGGGGAGGAGCAACGCCCCCTCTCTGA	1197

RESULT 11

44

356	TCGCTGGTCACTACGTTCATCTCGCGCCACAAGCGGATGCGGACCGGTGACCAACTTCTTAC	415
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416	ATCGCAACCTGGCGGCCACGGACGTGACCTTCTCTGTGCTCGCTTCA ^Δ CGGCC	475
301	CTGCTGTACCGCTGCCCGCTGGGTGCTGGGCACTTCA ^Δ TGTCGAAGTTCGTCAACTAC	360
476	CTGCTGTACCGCTGCCCGCTGGGTGCTGGGCACTTCA ^Δ TGTCGAAGTTCGTCAACTAC	535
361	ATCCAGCAGAGTCTCGGTGCAGGCCACGTGTGCCACTCTGACCGGCATAGTGTGCAGCCG	420
536	ATCCAGCAGAGTCTCGGTGCAGGCCACGTGTGCCACTCTGACCGGCATAGTGTGCAGCCG	595
421	TGGTACGTGACCGGTTCCTCGGTTCGCGCCCTGTGACCGCGCATAGTGTGCAGCCGCTG	480
596	TGGTACGTGACCGGTTCCTCGGTTCGCGCCCTGTGACCGCGCATAGTGTGCAGCCGCTG	655
481	GCTGTGACCTACAGATCTGGGTAGGCTCTGCGCGGGTGTCTGCGCGGTGCTCTGCCCTG	540
656	GCTGTGACCTACAGATCTGGGTAGGCTCTGCGCGGGTGTCTGCGCGGTGCTCTGCCCTG	715
541	CACCGCCTGTCA ^Δ CCCGGGCCGCGCCCTACTGTGCAGTGAGGCGCTTCCCA ^Δ CGCGGCCCTG	600
716	CACCGCCTGTCA ^Δ CCCGGGCCGCGCCCTACTGTGCAGTGAGGCGCTTCCCA ^Δ CGCGGCCCTG	775
601	GAGCGCGCTTCGACCTGTGACAACTGTGTGCGCTGTACTGTGTGCGCTGCTGTGCCACC	660
776	GAGCGCGCTTCGACCTGTGACAACTGTGTGCGCTGTACTGTGTGCGCTGCTGTGCCACC	835
661	TGCGCCTGTATGCGGCCATGCTGCGGCACCTGCGGCGGGTCTGCGGTGCGCCCGCGGCC	720
836	TGCGCCTGTGTATGCGGCCATGCTGCGGCACCTGCGGCGGGTCTGCGGTGCGCCCGCGGCC	895
721	GCCGATAGCGCCTGCAAGGGCAGGTGCTGCGAGAGCGCGCAGCGCGCTGCGGGCCCAAG	780
896	GCCGATAGCGCCTGCAAGGGCAGGTGCTGCGAGAGCGCGCAGCGCGCTGCGGGCCCAAG	955
781	GTCTCGGGCTGTGTGGCGCGCTGGTCTGTCTTTCGCGCGCTGTGTGGGCGCCCATCCAG	840
956	GTCTCGGGCTGTGTGGCGCGCTGGTCTGTCTTTCGCGCGCTGTGTGGGCGCCCATCCAG	1015
841	CTGTTCCTGTGTGCAAGGCGCTGGGCCCCCGCGGGCTCTGTGGACCA ^Δ CCACGAGCTAGCC	900
1016	CTGTTCCTGTGTGCAAGGCGCTGGGCCCCCGCGGGCTCTGTGGACCA ^Δ CCACGAGCTAGCC	1075
901	GCCTACCGCTTAAAGACTGGGCTCACTGTGATGTCTTACAGCAACTCCGGCTGAAACCCG	960
1076	GCCTACCGCTTAAAGACTGGGCTCACTGTGATGTCTTACAGCAACTCCGGCTGAAACCCG	1135
961	CTGCTCTACGGCTTCTGTGGGTCTGCACCTTTCGACAGGCTTCGCGCGGTGTGCCCCCTGC	1020
1136	CTGCTCTACGGCTTCTGTGGGTCTGCACCTTTCGACAGGCTTCGCGCGGTGTGCCCCCTGC	1195
1021	GCGCCGCGCGCCCCCGCGCGCGCGCGGACCTCTGGAACCCCGCAGCGCCACAC	1080
1196	GCGCCGCGCGCCCCCGCGCGCGCGGACCTCTGGAACCCCGCAGCGCCACAC	1255
1081	GCGGAGCTGCAACCGCTCTGGGCTCCACCCCGCGCCCCCGCAGGGCGCAGAAAGCCAGGGAGC	1140
1256	GCGGAGCTGCAACCGCTCTGGGCTCCACCCCGCGCCCCCGCAGGGCGCAGAAAGCCAGGGAGC	1315
1141	AGTGGGCTGGCGCGCGGCTGTGTGCTCTGTGGGGAGGACAAAGCCCTCTCTGA	1197
1316	AGTGGGCTGGCGCGCGGCTGTGTGCTCTGTGGGGAGGACAAAGCCCTCTCTGA	1372

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Job time : 1133 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 02:58:12 ; Search time 256 Seconds
(without alignments)
8311.489 Million cell updates/sec

Title: US-10-771-417-6
Perfect score: 1197
Sequence: 1 atgcacacgtggtacgtc.....aggacaacgccccctctctga 1197

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2.6/prodata/1/ina/5/COMB.seq.*
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9: /cgn2.6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	1197	100.0	1197	3	US-09-830-428A-6	Sequence 6, Appli
2	836.4	69.9	1191	3	US-09-830-428A-2	Sequence 2, Appli
3	187.8	15.7	1219	3	US-08-981-700A-3	Sequence 3, Appli
4	186.8	15.6	1365	3	US-08-999-112B-27	Sequence 27, Appli
5	186.8	15.6	1365	3	US-09-011-553-4	Sequence 4, Appli
6	186.2	15.6	1164	3	US-08-993-088A-6	Sequence 6, Appli
7	186.2	15.6	1164	3	US-08-993-424B-6	Sequence 6, Appli
8	186.2	15.6	1164	3	US-09-603-680-6	Sequence 6, Appli
9	184.6	15.4	1164	3	US-09-826-509-504	Sequence 504, App
10	175	14.6	1296	2	US-07-816-283-9	Sequence 9, Appli
11	175	14.6	1296	2	US-08-417-103-9	Sequence 9, Appli
12	175	14.6	1413	3	US-09-016-434-1321	Sequence 1321, Ap
13	173.4	14.5	1257	3	US-09-826-509-572	Sequence 572, App
14	171.2	14.3	1047	3	US-08-540-650B-6	Sequence 6, Appli
15	171.2	14.3	1050	3	US-09-826-509-502	Sequence 502, App
16	171.2	14.3	1053	3	US-09-016-434-1423	Sequence 1423, Ap
17	171.2	14.3	1882	3	US-08-540-650B-11	Sequence 11, Appli
18	171.2	14.3	3083	3	US-08-693-308-1	Sequence 1, Appli
19	168	14.0	1107	3	US-09-595-549-3	Sequence 3, Appli
20	168	14.0	1417	3	US-09-199-737-3	Sequence 3, Appli
21	168	14.0	1417	3	US-09-058-333A-3	Sequence 3, Appli
22	163.2	13.6	1796	2	US-07-816-283-11	Sequence 11, Appli
23	163.2	13.6	1796	2	US-08-417-103-11	Sequence 11, Appli
24	158.4	13.2	1275	3	US-08-916-247A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-830-428A-6
; Sequence 6, Application US/09830428A
; Patent No. 6699965
; GENERAL INFORMATION:
; APPLICANT: Takuya WATANABE
; APPLICANT: Yasuko TERAO
; APPLICANT: Yasushi SHINTANI
; APPLICANT: Tetsuya OHTAKI
; APPLICANT: Kimiko KANEHASHI
; APPLICANT: Chieko KITADA
; TITLE OF INVENTION: No. 6699965el G Protein Coupled Receptor Protein, DNA and its Lig
; FILE REFERENCE: 2001-0272A/WMC/01801
; CURRENT APPLICATION NUMBER: US/09/830,428A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: JP 10-305949
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: JP 11-027710
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: JP 11-057207
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: JP 11-276225
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 6
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Human
US-09-830-428A-6

Query Match 100.0%; Score 1197; DB 3; Length 1197;
Best Local Similarity 100.0%; Pred. No. 3.1e-180;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCACACGTGCTACGTCGACCCACCGCTCTCGGGGGCCACCGCCACGCTCC	60
Db	1	ATGCACACGTGCTACGTCGACCCACCGCTCTCGGGGGCCACCGCCACGCTCC	60
Qy	61	GGCTGCCCGGGCTGTGGCGCCAAACGCTCGACGGCCAGTCCCTTCGCGCGGGCGGTG	120
Db	61	GGCTGCCCGGGCTGTGGCGCCAAACGCTCGACGGCCAGTCCCTTCGCGCGGGCGGTG	120
Qy	121	GACGCTGTGCTGTGCGCGCTCTTCTTCGCGCGCGCTGTGCTGTGCGGGAAC	180
Db	121	GACGCTGTGCTGTGCGCGCTCTTCTTCGCGCGCGCTGTGCTGTGCGGGAAC	180
Qy	181	TGCTGGTTCATCTACGTCTATCTGCCGCCACACCGCATCGGACCGTTCAC	240

Db TCCTGGTTCATCTACGTTCATCTGCGCCACAAGCGATGCGGACCGTGACCAACTTCTAC 240
QY ATCCGCAACCTGGCGGCCACGAGCGTGACCTTCTCTGCTGCTGGTCCCTTACCGCC 300
Db ATCGCAACCTGGCGGCCACGAGCGTGACCTTCTCTGCTGCTGGTCCCTTACCGCC 300
QY CTGCTGTACCCGCTGCCCGGCTGGGTGCTGGCGCACTTCATGTGCAAGTTCGTCAACTAC 360
Db CTGCTGTACCCGCTGCCCGGCTGGGTGCTGGCGCACTTCATGTGCAAGTTCGTCAACTAC 360
QY ATCCAGCAGGTCTCGGTGCAGGCCACGTTGTCCTACTCTGACCGCCATGAGTGTGAGCCGC 420
Db ATCCAGCAGGTCTCGGTGCAGGCCACGTTGTCCTACTCTGACCGCCATGAGTGTGAGCCGC 420
QY TGTACGTGAGCGGTGTTCCCGTGGCGCCCTGACCGCCGCAAGCCCGCTGGCGCTG 480
Db TGTACGTGAGCGGTGTTCCCGTGGCGCCCTGACCGCCGCAAGCCCGCTGGCGCTG 480
QY GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGCGGTGCTGCGCGGTGCTGCCCGCTG 540
Db GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGCGGTGCTGCGCGGTGCTGCCCGCTG 540
QY CACCGCTGTCAACCGGCGCCGCGGCTTACTGCAAGTGGGCTTCCCGAGCGCGCCCTG 600
Db CACCGCTGTCAACCGGCGCCGCGGCTTACTGCAAGTGGGCTTCCCGAGCGCGCCCTG 600
QY GAGCGCGCTTCGCACTGTACAACCTGCTGGCGCTGACCTGCTGCTGCTGCTGCTGCTG 660
Db GAGCGCGCTTCGCACTGTACAACCTGCTGGCGCTGACCTGCTGCTGCTGCTGCTGCTG 660
QY TGGCGCTCTATGCGGCGCATGCTGGCGCATCTGGCGCGGTGCGCGCTGCGCGCGCC 720
Db TGGCGCTCTATGCGGCGCATGCTGGCGCATCTGGCGCGGTGCGCGCTGCGCGCGCC 720
QY GCCGATAGCGCCTGACAGGCGAGGTGCTGCGAGAGCGCGAGCGCGCGCGCGCGCAAG 780
Db GCCGATAGCGCCTGACAGGCGAGGTGCTGCGAGAGCGCGAGCGCGCGCGCGCGCAAG 780
QY GTCTCGCGGCTGTGGCGCGGTGCTGCTCTTCCGCGGCTGCTGGGCGCCATCCAG 840
Db GTCTCGCGGCTGTGGCGCGGTGCTGCTCTTCCGCGGCTGCTGGGCGCCATCCAG 840
QY CTGTTCTGTGTGCTGACGCGCTGGGCGCGCGGCTCTTGGCACCCACGAGCTAGCGC 900
Db CTGTTCTGTGTGCTGACGCGCTGGGCGCGCGGCTCTTGGCACCCACGAGCTAGCGC 900
QY GCCTACGCGCTTAAGACCTGGGCTCACTGCAATGCTTACAGCAACTCCGCGCTGAACCCG 960
Db GCCTACGCGCTTAAGACCTGGGCTCACTGCAATGCTTACAGCAACTCCGCGCTGAACCCG 960
QY CTGCTTACGCGCTTCTGGGCTCGCACTTCCGACAGGCGCTTCCGCGGCTTCCGCGCTG 1020
Db CTGCTTACGCGCTTCTGGGCTCGCACTTCCGACAGGCGCTTCCGCGGCTTCCGCGCTG 1020
QY GCG 1080
Db GCG 1080
QY GCGGAGCTGCAACCGCTTGGGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db GCGGAGCTGCAACCGCTTGGGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY AGTGGGCTGGCG 1197
Db AGTGGGCTGGCG 1197

RESULT 2
US-09-830-428A-2
; Sequence 2, Application US/09830428A
; Patent No. 6699965
; GENERAL INFORMATION:

; APPLICANT: Takuya WATANABE
; APPLICANT: Yasuo TERAO
; APPLICANT: Yasuhiro SHINTANI
; APPLICANT: Tetsuya OHTAKI
; APPLICANT: Kimiko KANERASHI
; APPLICANT: Chieko KITADA
; TITLE OF INVENTION: No. 6699965el G Protein Coupled Receptor Protein, DNA and its Lig
; FILE REFERENCE: 2001-0272A/WMC/01801
; CURRENT APPLICATION NUMBER: US/09/830,428A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: JP 10-305949
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: JP 11-027710
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: JP 11-057207
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: JP 11-276225
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 2
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Rat
; US-09-830-428A-2

Query Match 69.9%; Score 836.4; DB 3; Length 1191;
Best Local Similarity 82.6%; Pred. No. 1.9e-123;
Matches 957; Conservative 0; Mismatches 201; Indels 0; Gaps 0;
Qy 1 ATGCACACCGTGGCTACGTCCGGACCCAAACGCGCTCTGGGGGGCACCGGCAACGCTCC 60
Db 1 ATGCGCGCAGAGCGGACGTTGGGTCCGAACGTGAGCTGGTGGGCTCGCTCCAAAGCTTCG 60
Qy 61 GGCTGCCCGGGCTGTGGCGCCAAACGCTCGGACGGCCAGTCCCTTCCGCGCGGGCGGTG 120
Db 61 GGATGCCCGGGCTGCGGTGTCAATGCTCGGATGGCCAGGCTCCGCGCAAGGCCCTCGT 120
Qy 121 GAGCCCTGGCTGCTGCCGCTCTTCTTCCGCGCGCTGATGCTGTGGGCTTGGTGGGGAAC 180
Db 121 GATGCTGGCTGGTGGTCCCTGTTTTCGCTGCCCTAATGTTGCTGGGGTAGTCCGGNAAC 180
Qy 181 TCGCTGTGTCATCTACGTCACTGCGGCCCAAGCCGATGCGGACCGGTGACCACTTCTAC 240
Db 181 TCACTGTGTCATCTTCGTTATCTGCGGCCAAGCACATGACAGACCGTCAACCAATTTCTAC 240
Qy 241 ATGCCCAACCTGGCGGCCACGAGCTGACCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 ATCGCTAACCTGGCGGCCACAGATGTCACTTTCCTTCTGTGCTGCTGCTGCTGCTGCTG 300
Qy 301 CTGCTGTACCCGCTGCCCGGCTGGGTGCTGGGCGACTTCATGTGCAAGTTCGTCAACTAC 360
Db 301 CTCTCTATCGCTGCCCACTGGGTGCTGGGAGACTTCATGTGCAAAATTCGTCAACTAC 360
Qy 361 ATCCAGCAGGTCTCGGTGCAGGCCACGTTGCCCTCTGACCCGCCATGAGTGTGAGCCGC 420
Db 361 ATCCAGCAGGTCTCGGTGCAGGCCACATGTCCTATTTGACAGCATGAGTGTGAGCCGC 420
Qy 421 TGTACGTGAGGTGTTCCCGTTCGCGCCCTGACCGCGCCAGCGCCCGCGCTGGCGCTG 480
Db 421 TGTACGTGAGTGTGTTCCCGTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGCGGTGCTGCGCGCGGTGCTGCGCGCTG 540
Db 481 ACTGTGAGCTTAGCATCTGGGTGGGTTCGAGCTGTTTCGCGCCCGGTGCTGGCTCTG 540
Qy 541 CACCGCTGTCAACCGGCGCGCGCTTATGCAAGTGGGCTTCCCGAGCGCGCGCTG 600
Db 541 CACCGCTGTGCGCGCGCGCTCAACCTACTGCAAGTGGGCTTCCCGAGCGCGCTG 600
Qy 601 GAGCGCGCTTCGCACTGTACAACCTGCTGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 GAGCGCGCTTCGCGGCTCTCAACCTGCTGGCGCTTATACCTGCTGCTGCTGCTGCTGCTG 660

[illegible]

Db 1047 GGGGGCCCTTCGTCTGCCCGCGGCTTCC 1077

RESULT 7

US-08-993-424B-6

; Sequence 6, Application US/08993424B

; Patent No. 6337206

; GENERAL INFORMATION:

; APPLICANT: Tan, Carina

; APPLICANT: Kolakowski, Lee F., Jr.

; TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALR2 AND

; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merck & Co., Inc.

; STREET: P.O. Box 2000, 126 E. Lincoln Ave.

; CITY: Rahway

; STATE: NJ

; COUNTRY: USA

; ZIP: 07065-0900

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSeq For Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/993,424B

; FILING DATE: 18-DEC-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/033,851

; FILING DATE: 27-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Heber, Sheldon O.

; REGISTRATION NUMBER: 38,179

; REFERENCE/DOCKET NUMBER: 19846NP2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 732-594-1958

; TELEFAX: 732-594-4720

; TELEX:

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1164 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

US-08-993-424B-6

Query Match 15.6%; Score 186.2; DB 3; Length 1164;

Best Local Similarity 51.4%; Pred. No. 4.3e-21;

Matches 540; Conservative 0; Mismatches 468; Indels 43; Gaps 3;

Qy 121 GAGCGCTGGCTCGTGGCGCTCTTCTTCGCGCGCGGTGATGCTGCTGGCGCTGGTGGGGAAC 180

Db 70 GAGCGGTATCGTGGCCCTGCTCTTCGCGCTCATCTTCTCGTGGGACCGTGGGCAAC 129

Qy 181 TCGCTGTGTCATCGTCATCTGCGGCCAAGCCGATGCGGACCGTGACCACTTCTAC 240

Db 130 ACGCTGTGCTGGCGGTGCTGCTGCGCGGGCGCCAGCGGTGACACTCAACACTGTTC 189

Qy 241 ATGCCAACCTGGCGGCACGAGCTGACCTTCTCTGTGCTGCTGCTCCCTTCACGGCC 300

Db 190 ATCCTTAACCTGGCGGTGGCCGACCTGTGTTTTCATCTGTGCTGCTGCGCTCCAGGCC 249

Qy 301 CTGCTGTACCCGCTGCCCGCTGGGTGCTCGGGCGACTTCATGTGCAAGTTCGTCACTAC 360

Db 250 ACCATCTACACCTGGACGGCTGGGTGTTCCGGTTCGCTGCTGTGTGCAAGGGGTGCACTTC 309

Qy 361 ATCAGCAGGTCTCGGTGACGGCCACGTGTGCCACTCTGACCGGCATGAGTGTGACCGC 420

Db 310 CTATCTTCTCACCATGCAAGCGACGACTTTCACGCTGGCGCGCGTCTCCCTGGACAGG 369

	Qy	421	TGTTACTGTACGGTGTTCCTCGTTCGGCGCCCTGTGCACGCCGCGCAGCCCCCGCCTGGCGCTG	480
	Db	370	TATCTGCCCATTCGGCTAACCCGCTGCACTCCCGAGTGTGCAGCGCTCGAAACGGCGCTG	429
	Qy	481	GCTGTACGCTTCAGCATCTGGTAGGCTCTGCGSCGGTGTCGCGCGGTGCTCGCCCTG	540
	Db	430	GCAGCCATCGGGCTCATCTGGGGCTGTGCTGCTCTTCGSGGCCCTACCTTAGGTTAC	489
	Qy	541	CACGGCTGTCAACCGGGCGCGGCCCTACTGTGAGTAGAGCCCTTCCCAGCCGCGCCCTG	600
	Db	490	TACCGCCAGTCGCAGCTGGCCAACTTACCGTGTGCCATTCCCGGTGGAGCGCCCTCGC	549
	Qy	601	GAGCGCGCCTTCGCACTGTACAACCTGCTGGCGCTGTACCTGTGCGCGCTGCTGCGCAC	660
	Db	550	CGCGCGCCCATGGACATCTGCACCTTCGTCTTTCAGCTACCCTGCTTCGTGCTGCTCTC	609
	Qy	661	TGCGCTGCTATGGGGCGCATGCTGCGGCACCTCGGGCGGGTTCGCGCGTGCGCCCGCGCC	720
	Db	610	GBCCTGACCTACGCGCGGACCTTGGCTTA CCTCTGGCGCGCGTGG-----	655
	Qy	721	GCCGATAGCGCCTTCAGAGGGGCAAGTGTCTGGCAGAGCGCGCAGCGCCGTGCGGGCCAAG	780
	Db	656	-----ACC CGTGGCGCGGGCTCGGGTGCCCGCGCGCCAA--	692
	Qy	781	GTCTCGCGGCTGTGTGGCGCGGTGGTCTGTGTTCTTCGCGCGCTGTGCGGCGCCCATCCAG	840
	Db	693	-----GCGCAAGGTGTACACG CATGATCTCATCTGTGCGCGGTCTTCTGCTCTGTGTGG	747
	Qy	841	CTGTTCTGTGTCTAGCGGCGCTGGGCGCCCGCGGGCTCTGGCACCCACCGCAGCTACGCC	900
	Db	748	ATGCCCCACACGCGCTCATCTCTGCGGTGTGGTTCTGGCCAGTTCCCGCTCAGCGCGCC	807
	Qy	901	GCCTACCGGCTTAAGACCTGGGCTCACTGTGATGTCTTACAGCAACTCCGGGCTGAACCCG	960
	Db	808	ACTTATGGGCTTCGCATCTCTCGCACCTGGTCTCTACGCCA ACTCTCGGTCAACCCC	867
	Qy	961	CTGCTCTACGCTTTCCTGGGCTTCGCATCTTCGCA GAGGCTTCGCGCGGCTGTGCGCCCTGC	1020
	Db	868	ATCGTTTACGCGCTGTGCTC CAAGCATTTCCGAAAGGCTTCCGACGATCTGCGCGGGC	927
	Qy	1021	GCGCGCGCGCCCGCGCGCCCGCGCGCCCGGACCCCTCGGACCCCGCAGCGCCCAACAC	1080
	Db	928	CTGCTGGGCGGTGCCCAAGGCGGAGCCTCTGGGCGGTGTGTGCTGTGCGC-GCGGGGCAC	986
	Qy	1081	GCGGAGCTGCACCCGCTGGGGTCCACCCCGGCCCGCCCGAGCCCTCGGACCCCGCAGCGCCACAC	1140
	Db	987	CCACAGTGGCAGCGTTGTGGAGCGGAGTCCAGCGACCTGTTGCACATGAGCGGGCGC	1046
	Qy	1141	AGTGGGCTGGCCGCGCGGGCTGTGCGTCC	1171
	Db	1047	GGGGGCGCTTCGTCTCCTCGCCCGCGCGCTTCC	1077

RESULT 8

US-09-603-580-6
; Sequence 6, Application US/09603680
; Patent No. 6544753
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; Sullivan, Kathleen
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
; NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

Qy 721 GCCGATAGCGCCTGTCAGGGCAGGTGCTGGCAGAGCGCGCAGCGCGCTCGGGCCCAAG 780
Db 656 -----ACCCGGTGGCGCGGCTCGGGTGGCGGCGGCCAA- 692
Qy 781 GTCTCGGGCTGGTGGCGCGCTGCTGCTCTTTCGCGCGCTGCTGGGGCCCCATCCAG 840
Db 693 -----GGCAAGGTGACACGATGATCTCATCGTGGCGCGGCTCTTCTGCTCTGCTGG 747
Qy 841 CTGTTCTGTGTGCTGACAGCGCTGGGCCCGCGCGGCTCTTGGCACCCAGCAGCTAGGCC 900
Db 748 ATGCCCAACACAGCGCTCATCTCTGCTGTGGTTCGGCGAGTTCCTCGCTCACCGCGCC 807
Qy 901 GCCTACCGCTTAAGACCTGGGCTCACTGCACTGCTTACAGCAACTCCGCGCTGAACCCG 960
Db 808 ACTTATGGCTTCGATCCTCTCGCACCTGTCTCTTACGCCAACTCTCTGGGTCAACCCC 867
Qy 961 CTGCTCTACGCTTCTCTGGGCTCGCACTTCGACAGGCTTCGCGCGGCTGTCGCCCTGC 1020
Db 868 ATCGTTTACGGGCTGGTCTCAAGCACTTCGCGCAAGGCTTCGACGATCTGGCGGGC 927
Qy 1021 GCG 1080
Db 928 CTGCTGGCGCTGCG 986
Qy 1081 GCGGAGCTGACCGCTGGGCTCCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db 987 CCACAGTGGCAGCGTGTGGAGCGGAGTCCAGCGACCTGTTGCACATGACGAGGCGCG 1046
Qy 1141 AGTGGCTGGCG 1171
Db 1047 GGGGGCCCTTCTGCTCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1077

RESULT 9
US-09-826-509-504
; Sequence 504, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 504
; LENGTH: 1164
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-504

Query Match 15.4%; Score 184.6; DB 3; Length 1164;
Best Local Similarity 51.3%; Pred. No. 7.6e-21;
Matches 539; Conservative 0; Mismatches 469; Indels 43; Gaps 3;

Qy 121 GACCGCTGGCTCGGCGCGCTCTTTCGCGCGGTGATGCTGCGGCGCTGGGCGCTGGTGGGAC 180
Db 70 GAGCGGTGTCATCGTGGCGCGCTCTTTCGCGGTCTATCTTCTGCTGGGCGCGCTGGGCAAC 129
Qy 181 TCGCTGGTCTATCTAGTCTATCTGCGCGCACCAAGCGATGCGGACCGGTGACCAACTTCTTAC 240
Db 130 ACGTGGTGTGGCGGTGCTGCTGCGCGCGCGCGCGCGCGGTGACCAACTTCTTAC 189
Qy 241 ATCGCCCACTGGCGCGCACCGAGTACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 190 ATCCTTAACCTGGCGGTGGCGCGAGCTGTGTTTCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 249

Qy 301 CTGCTGTACCGCTGCCCGCTGGGTGCTGGGCGACTTTCATGTGCAAGTTCGTCAACTAC 360
Db 250 ACCATCTACACCTTGGACGGCTGGGTGTTTGGCTCGCTGCTGTGTCAGAGCGGTGACATTC 309
Qy 361 ATCCAGCAGGTTCCTGGTGCAGGCCACGTGTGCCACTCTGACCCGCCATGAGTGTGAGACGC 420
Db 310 CTATCTTCTCACCATGACCGCGCAGCAGCTTACCGTGGCGCGGCTCTCCCTGAGACAG 369
Qy 421 TGGTACGTGAGGTGTTCCGTTGGCGCGCTGACCGCGCAGCGCCCGCTGGCGCTG 480
Db 370 TATCTGCCATTCGCTTACCCGCTGCACTCCGCGAGCTGGCGCAGCTCGAAACGCGCTG 429
Qy 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGGCGCGGTGTCTGGCGCGGTCTGCGCCCTG 540
Db 430 GCAGCATCGGCTCATCTGGGGGCTGCTGCTCTTCTCCGGGCGCTTACCTGAGCTAC 489
Qy 541 CACGCGCTGTACCCCGCGCGCGCGCTA CTGACAGTGAAGGCTTCCCGACGCGCGCGCTG 600
Db 490 TACCGCAGTCCGAGCTGGCGCAACCTGACCGTGTGCCATCCCGGTGGAGCGCGCCCTCGC 549
Qy 601 GAGCGCGCTTGCACATGTACACCTGCTGGCGCTGTACCTGCTGCGCGCTGCTGCGCAC 660
Db 550 CGCGCGCGCATGACATCTGCACCTTCTGCTCTTACAGTACCTGCTTCTGCTGCTGCTG 609
Qy 661 TGCGCTGCTATGCGGCGCATGTGCGGCACCTGGGCGGGTTCGCGCTGCGCGCGCGCG 720
Db 610 GGCCTGACCTACGCGCGCACCTTGGCTACTCTTGGCGCGCGCTG----- 655
Qy 721 GCCGATAGCGCCTGACGGGCGAGGTGCTGGCAGAGCGCGCAGCGCGCTGCGGCGCAAG 780
Db 656 -----ACCCGGTGGCGCGCGGCTCGGGTGGCGCGCGCGCGCGCGCGCGCGCGCG 692
Qy 781 GTCTCGCGGCTGGTGGCGCGGTGCTGCTCTTTCGCGCGCTGCTGGGCGCGCGCGCGCG 840
Db 693 -----GCGCAAGGTGAAACGCATGATCTCATCTGCGCGCGGCTCTTCTGCTCTGCTGG 747
Qy 841 CTGTTCTGCTGTGTCAGGCGCTGGGCGCGCGCGGCTCTTGGCACCCACCGCAGCTAGCGCC 900
Db 748 ATGCCCAACACAGCGCTCATCTCTGCTGTGGTTCGGCCAGTTCGCGCTCACGCGCGCC 807
Qy 901 GCCTACCGCTTAAGACCTGGGCTCACTGATGCTTCTTACAGCAACTCCGCGCTGAACCCG 960
Db 808 ACTTATGGCTTCGATCCTCTGCACTGCTCTCTTACGCGCAACTCTCTGCTCAACCCC 867
Qy 961 CTGCTCTACGCTTCTCTGGGCTCGCACTTCGACAGGCGCTTCCGCGCGCTGCGCCCTGC 1020
Db 868 ATCGTTTACGCGCTGGTCTCAAGCACTTCGCGCAAGGCTTCGACGATCTGGCGGGC 927
Qy 1021 GCG 1080
Db 928 CTGCTGGCGCTGCG 986
Qy 1081 GCGGAGCTGACCGCTGGGCTCCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db 987 CCACAGTGGCAGCGTGTGGAGCGGAGTCCAGCGACCTGTTGCACATGACGAGGCGCG 1046
Qy 1141 AGTGGCTGGCG 1171
Db 1047 GGGGGCCCTTCTGCTCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1077

RESULT 10
US-07-816-283-9
; Sequence 9, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Subumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

; NAME/KEY: CDS
; LOCATION: 28..1281
US-08-417-103-9

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Query Match      14.6%; Score 175; DB 2; Length 1296;
Best Local Similarity 53.8%; Pred. No. 2.5e-19;
Matches 520; Conservative 0; Mismatches 405; Indels 42; Gaps 6;

Qy 79 GCCAACGCTCGGACGGCCCAAGTCCCTTTCGCGCGGGCGGTGGACGCTGCTGCTGCTGCGG 138
Db 112 GGCACAGTGTGCGCGGGCCCAAGCCCGCAGGCTGCGCGTCACTGGGTTCTGATCCCC 171
Qy 139 CTCCTTTTCGCGGCGCTGATGCTGCTGGGCTTGTGGGAACTCGCTGGTCACTACGTC 198
Db 172 CTGGTCTACCTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 231
Qy 199 ATCTGCGCCACAGCGATCGGACCGTGGACCACTTCTACATCGCCAGCTGGCGCC 258
Db 232 GTCTGCGGCACAGCGCCAGCCCTTCAGTCAACACGCTTACATCCTCAACCTGGCGTG 291
Qy 259 ACGGACGTGACCTTCTCTGCTGCTGCCCTTTCAGCGCCCTGCTGTACCCGCTGCC 318
Db 292 GCCAGAGCTCTTCATGCTG---GGCTGCCCTTCTGCGCGCCAGAACGCTGCTGCC 348
Qy 319 GGTGGGTGCTGGGCGACTTCATGTGCAAGTTCTGTCACATCACTACAGAGGTCTCGGTG 378
Db 349 TACTGGCCCTTCGGCTCCCTCATGTGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408
Qy 379 CAGGCCAGTGTGCCACTCTACAGCCCATGAGTGTGGACCGCTGCTGCTGCTGCTGCTGCTGCT 438
Db 409 TTCACAGCATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
Qy 439 CCGTTGCGCGCCCTGCAACCGCGCACGCGCCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 498
Db 469 CCCACCGCTCGGCCGCTGCGGCACAGCTCGGTGGCGCCGACAGCTCAGGCGCGCTGTG 528
Qy 499 TGGTAGGCTCTGCGGCGGTGTGCGCGCGGTGTGCGCGGTGTGCGCGGTGTGCGCGGTGTGCGCGGTG 558
Db 529 TGGGTGGCTCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 588
Qy 559 CCGCGCGCTACTGACGTAG---GCCCTCCACGCGCGCGCTGAGCG---CGCTTTCGA 615
Db 589 ATGAGCACTCCACATGCACTGCGCGCGAGCGCGCGCGCTGCGCGCGCTGCGCGCGCTTATC 648
Qy 616 CTGTACAACTGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
Db 649 ATCTACAGCGCGCACTGGGCTTCTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
Qy 676 GCCATGTCGCCCACTGGGCGGGGTGCGCGCGGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 735
Db 709 CTCATCGTGTGAAGTGGC-----TCAGTGGGCGCGGGTGTGGGCAACCCCTC 758
Qy 736 CAGGGGAGGTGCTGGGAGAGCGGCGCGCGCTGCGGGGCAAGTCTCGCGCTGGTG 795
Db 759 GTGCCAGCGCGCGCGCGCTCCGAAC-----GCAGGGTACCGCATGGTG 804
Qy 796 GCGGCGGTGCTGCTGCTTTCGCGCGCTGCTGGGCGCCATCCAGCTGCTTCTGCTGCTGCTGCTGCTG 855
Db 805 GTGGCGGTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
Qy 856 CAGGCGTGGCGCGCGCGGTCTTGGGCAACCGACAGCTACGCGCGCTACGCGCTTAAG 915
Db 865 AACGTGGTGTGCCACTGCCGAGGAGC-----CTGCTTCTTTGGGCTCTAC 912
Qy 916 ACCTGGGCTCACTGATGCTTACAGCACTCGGGCTGAGACCGCTGCTTACGCTTC 975
Db 913 TTCCTGGTGGTGGCGCTGCTTATGCCAACAGCTGTGCCAACCCCATCTTTTATGGCTTC 972
Qy 976 CTGGGCTGCCATTTCCGACAGGCTTCCGCGCGGTCTGCCCTTGGCGCGCGCGCGCGCGCGCGCGCGCG 1035
Db 973 CTCCTCCTACCGCTTCAAGAGGGCTTCCGAGAGGTCTGCTGCGGCGCTCCCGCGGTG 1032
Qy 1036 GCGCGCC 1042
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Db 1033 CGCAGCC 1039

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RESULT 12
US-09-016-434-1321
; Sequence 1321, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1321:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g338498
; US-09-016-434-1321
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Query Match      14.6%; Score 175; DB 3; Length 1413;
Best Local Similarity 53.8%; Pred. No. 2.5e-19;
Matches 520; Conservative 0; Mismatches 405; Indels 42; Gaps 6;

Qy 79 GCCAACGCTCGGACGGCCCAAGTCCCTTTCGCGCGGGCGGTGGACGCTGCTGCTGCTGCGG 138
Db 182 GGCACAGTGTGCGCGGGCCCAAGCCCGCAGGCTGCGCGTCACTGGGTTCTGATCCCC 241
Qy 139 CTCCTTTTCGCGGCGCTGATGCTGCTGGGCTTGTGGGAACTCGCTGGTCACTACGTC 198
Db 242 CTGGTCTACCTGGTGTGTGCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
Qy 199 ATCTGCGCCACAGCGATCGGACCGTGGACCACTTCTACATCGCCAGCTGGCGCC 258
Db 302 GTCTGCGGCACAGCGCCCTTCAGTCAACACGCTTACATCCTCAACCTGGCGTG 361
Qy 259 ACGGACGTGACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 318
Db 362 GCGGACAGCTCTTCATGCTG---GGCTGCCCTTCTGCGCGCCAGAACGCGCTGCTCC 418
Qy 319 GGTGGGTGCTGGGCGGACTTCATGTGCAAGTTCGTCAACTACATCCAGCAGGTCTCGGTG 378
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Db	419	TACTGGCCCTTCGGCTCCCTCATGTGCGGCTGGTCACTGGCGGTGGATGGCATCAAC	478
Qy	379	CAGGCCACGCTGTGCACACTCTTGACCGCATGAGTGTGACCGCTGGTAGCTACGTGGTTC	438
Db	479	TTCAACAGCATATTTCTGCCTAGCTGTATGAGCGTGGACCGCTACCTGGCGGCTGGTACAT	538
Qy	439	CCGTTGGCGGCTCTGCACCGCGCACCGCCCGCTGGCGTGTGTGACGCTCAGCATC	498
Db	539	CCCAACCGCTCGGCCCGCTGGCGCACAGCTCCCGTGGCCCGCAGCGGTCAAGCGGGCTGTG	598
Qy	499	TGGGTAGGCTCTGGCGGCGGTGTCTGCGCGCGGTGTCTGCCCTGCAACGCCCTGTCAACCGGG	558
Db	599	TGGGTGGCCTCAGCCGTGGTGGTCTGCCCGTGGTGTCTTCTCGGAGTGCCTCCCGCGC	658
Qy	559	CCGCGCGCTACTGCAGTGAG--GCCCTTCCACAGCCGCGGCTGGAGCG--CGCCTTCGCA	615
Db	659	ATGAGCACTTGCACATGCAATGTCGCCGAGCGCGCGCGCTGGCAGCGCGCTTCATC	718
Qy	616	CTGTACAACTGTGGCGCTGTACTGCTGCGCGTGTCTGCGCACCTCGCGCTGTATGCG	675
Db	719	ATCTACAGCGCGCACTGGGCTTCTTCGGGCCGTGCTGTGTATCTGCTCTGTCTACCTG	778
Qy	676	GCCATGCTGGGCCACCTTGGGCGGGTTCGCGTGCGCCCGCGCCGATAGCGCCCTG	735
Db	779	CTCATCTGTGTGAAGTGCGC-----TCAGCTGGGCGCGGGTGTGGGCACCCCTC	828
Qy	736	CAGGGGAGGTGTGTGGCAGACGCGCAGCGCCGTGCGGGCCAAAGTCTTCGCGGCTGGT	795
Db	829	GTGCCAGCGCGCGCGCTCCGAAC-----GCAGGGTCACGCGCATGGTG	874
Qy	796	GCGGCCGTGTCTGTCTCTTCGCGCGCTGTGGGCCCCATTCACGTGTTCCTGGTGTGCTG	855
Db	875	GTGCGCGTGTGGCGCTCTTGTGCTCTGTGTGATGCGCTTCTACGTGCTCAACATCGTC	934
Qy	856	CAGCGCTGGGCCCCGGGGCTCTTGACCCCAACGACGTACGCGGCTACGGGCTTAAG	915
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Qy	916	ACCTGGGCTCACTGCATGTCTACAGCAACTCCCGGTGAAACCGGTGCTCTACGCGCTTC	975
Db	983	TTCTGTGTGGCGCTGCCCTATGCCAACAGCTGTGCGAACCCCATCTCTTATGGCTTC	1042
Qy	976	CTGGGCTCGCACTTCCGACAGGCGCTTCGCGCGCTCTGCCCTCTGCGCGCGCGCGCCCC	1035
Db	1043	CTCTCTTACCGCTTCAAGCAGGGCTTCGACAGGGTCTGCTGCGGCGCTCCCGCGGTG	1102
Qy	1036	CGCCGCC	1042
Db	1103	CGCAGCC	1109

RESULT 13
US-09-826-509-572
Sequence 572, Application US/09826509
Patent No. 6806054
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826.509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 572
LENGTH: 1257

	Query Match	14.58;	Score 173.4;	DB 3;	Length 1257;
	Best Local Similarity	53.78;	Pred. No. 4.4e-19;		
	Matches 519;	Conservative 0;	Mismatches 406;	Indels 42;	Gaps 6;
Qy	79	GCCAAACGCTCGAGACGGCCAGTCCCTTCGCGCGGGCGCGTGAGACGCTCGCTGCTGTCGGC 138			
Db	85	GGCAACGTCGCGGGGCCCAAGCCGGCAGGGCTGGCCGTCAGTGGCGTTCATGATCCCC 144			
Qy	139	CTCTTCTTCGCGGCGTGATGCTGCTGGCGCTGGTGGGAACTCGCTGGTGCATCTACGTC 198			
Db	145	CTGGTCTACCTGTGTGTGGTGGTGGCGCTGTGGGTAACTCGCTGGTCACTATATGTG 204			
Qy	199	ATCTGCCGCGCACAGCCGATGCGGACCGTGACCAACTTCTACATCGCAACCTGGCGGCCC 258			
Db	205	GTCCTGGGCACACGGCCAGCCCTTCAGTCACCAACGCTACATCTCAACCTGGCGCGTG 266			
Qy	259	ACGGACGTGACCTTCCTCTGTGTGCGTGCCTCCCTTCACGGCCCTGTGTACCCGCTGCC 318			
Db	265	GCCGACGAGCTTCATGCTG---GGCTGCGCTTCCTGGCGCCCAAGACGCCCTGTGCC 321			
Qy	319	GGCTGGGTGCTGGCGGACTTCATGTGCAAGTTCGTTCACATACACGACAGGTCTCGGTG 378			
Db	322	TACTGGCCCTTCGGCTCCCTCATGTGCGGCTGGTTCATGGCGGTGGATGGCATCAACCA 381			
Qy	379	CAGGCCAGGTGTCACACTCTGACCGCATAGTGTGGACCGCTGGTACGTGACGGTGTTC 438			
Db	382	TTACACGACATATTCCTGCGCTGACTGTCTAGGCGTGGACCGCTACCTGGCGCGTGTACAT 441			
Qy	439	CCGTTGGCGGCCCTTCGACCCGCGCAGCCCGCGCTGGCGCTGGCTGTGTACGCTCAGCATC 498			
Db	442	CCACCGCTCGGCCCGCTGGCGCACAGCTCCGGTGGCGCGCAGGTGAGCGGGCTGTG 501			
Qy	499	TGGGTAGGCTCTCGCGCGGTGTCTGGCGCGGTGTCTGCCCTGACCGCCTGTCAACCGGG 558			
Db	502	TGGGTGGCTCAGCGGTGGTGGTGTGCTGCCCGTGGTGGTCTTCTCGGAGTGGCCCGGCG 561			
Qy	559	CCGCGCGCTACTGCACTGAG--GCCTTCCGACGCGCGCCCTGGAGCG--CGCTTCGCA 615			
Db	562	ATGAGCACTTGCACATGCAAGTGGCGCGACCGCGCGCGCTTGGGAGCGCGCTTCATC 621			
Qy	616	CTGTACAACTGTGGCGGTATCCTGCTGCCGTGCTCGCCACTTCGCGCTGTATATGCG 675			
Db	622	ATCTACAGCGCGCATGGGCTTCTTCGGGCGCTGCTGTGTATCTGCTCTGTACTCTG 681			
Qy	676	GCCATGTGGGCCACCTGGGCGGGTCCGCTGGCGCCCGCGCGCGCGATAGCGCCCTG 735			
Db	682	CTCATCGTGGTGAAGTGGCGC-----TCAGCTGGGCGCGGGTGTGGGACACCTC 731			
Qy	736	CAGGGGAGGTGCTGGCAGAGCGCGCAGGCGCGTGGGGGCCAAGGTCTCGCGGCTGGT 795			
Db	732	GTGCCAGCGCGCGCGCTCCGAAC-----GCAGGGTCAAGCGCATGGGTG 777			
Qy	796	GCGGCGGTGCTGCTCTTCGCGCGCTGCTGGGGCCCATCAGCTGTTCCTGGTGTGCTG 855			
Db	778	GTGGCCGCTGTGGGCTCTTCGTGTCTGTGTGATGTCCTTCTACGTGCTCAACATGCTC 837			
Qy	856	CAGCGCTGGGCGCGCGGCTCTGTGGACCCACGACAGTACGCGGCTTACGGGCTTAAG 915			
Db	838	AACTGGTGTGCCACTGCGCGAGGAGC-----CTGCTTCTTTGGGCTCTAC 885			
Qy	916	ACCTGGGCTCATGTGCATGTCTTACAGCACTCCGCGCTGAACCGCTGTCTACGCGCTTC 975			
Db	886	TTCTGTGTGGGCGTGGCTTATGCCAAAGCTGTGGCAACCCCACTCTTTATGGCTTC 945			
Qy	976	CTGGGCTCGCACTTCGACAGGCTTCCGCGGGTCTGCCCTTGTGGCGCGCGCGCGCCCC 1035			
Db	946	CTCTCTACCGCTTCAAGCAGGGGCTTCCGACAGGGTCTGTGTGGGCGCTCCGCGCGTGTG 1005			
Qy	1036	CGCGGCC 1042			

Db 1006 CGCAGCC 1012

|||||

RESULT 14

US-08-540-650B-6

; Sequence 6, Application US/08540650B

; Patent No. 6399325

; GENERAL INFORMATION:

; APPLICANT: HINUMA, Shuji

; APPLICANT: FUJII, Ryo

; APPLICANT: FUKUSUMI, Shoji

; APPLICANT: OHTAKI, Tetsuya

; APPLICANT: HOSoya, Masaki

; APPLICANT: OHGI, Kazuhiro

; APPLICANT: ONDA, Haruo

; TITLE OF INVENTION: GALANIN RECEPTOR PROTEIN, PRODUCTION AND USE THEREOF

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: US

; ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/540,650B

FILING DATE: 11-OCT-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 7-134412

FILING DATE: 31-MAY-1995

APPLICATION NUMBER: 6-326610

FILING DATE: 28-DEC-1994

APPLICATION NUMBER: 6-247599

FILING DATE: 13-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: RESNICK, DAVID S

REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 45901

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1047

TYPE: Nucleic acid

STRANDEDNESS: Double

TOPOLOGY: Linear

MOLECULE TYPE: cDNA

FEATURE:

; IDENTIFICATION METHOD: S

US-08-540-650B-6

Query Match 14.3%; Score 171.2; DB 3; Length 1047;

Best Local Similarity 58.2%; Pred. No. 9.9e-19;

Matches 346; Conservative 0; Mismatches 233; Indels 15; Gaps 2;

Qy 115 GCCGTGAGCGCTGGCTCGTGGCGCTCTTCTGCGGCGCTGATGCTGCGGCTGGT 174

Db 88 GCGGTGAGAACTTCTGTCACCGTGGTGTGTTTGGCGCTGATCTTGGCGCTGGGCTGCTG 147

Qy 175 GGGAACTCGCTGGTCTAGCTATCTGCGGCCACAAAGCCGAT-----CGGACCGGTG 228

Db 148 GGCACACCTTAGTATCACCGTGTGGCGGCGACGAGCCGGGAGCCGCGGAGCACC 207

Qy 229 ACCAACTTCTATGCGCAACCTGCGGCGCCAGGACGTGACCTTCTCTGCTGCTGCTC 288

Db 208 ACCAACTTCTATGCGCAACCTGCGGCGCCAGGACGTGACCTTCTCTGCTGCTC 267

Qy 289 CCCTTACGCGCCCTGCTGTATCCCGCTGCCCGGCTGGGTGTGGGGGAGCTTCTCATGTGCAAG 348

Db 208 ACCAACTTCTATGCTTCAACCTGAGCATCGCGACCTGCGCTACCTGCTCTTCTGCAATC 267

Qy 289 CCCTTACGCGCCCTGCTGATACCGCTGCCCGCTGGGTGTGGCGGAGCTTCTCATGTGCAAG 348

Db 268 CCCTTCCAGGCCACCGTGTAGCGGCTGCCACCTGGGTGTGGCGGCTTCTCATGTGCAAG 327

Qy 349 TTCGTCAACTACATCCAGCAGGTCTCGGTGCAGGCCACGTTGTGCCACTCTGACGCCCATG 408

Db 328 TTCATCCACTACTTCTTTCACCGTGTCCATGCTGGTGAAGCATCTTTCACCCCTGGCCGCGATG 387

Qy 409 AGTGTGACCGCTGGTACGTGACGGTGTTCGGTTGGCGGCGCTGACACCGCGCAGCCGCC 468

Db 388 TCCGTGGACCGCTACGTGGCCATCGTGCACCTCGCGGCGCTCCTCTCCCTCAGGGTGTCC 447

Qy 469 CGCTGCGCGTGGCTGTGACGCTCAGCATCTGGGTAGGCTCTGCGGCGGTGTCTGCGCGC 528

Db 448 CGCAACCGCTGTGGCGGTGGCTGTCATCTGGCGGCTGTCCATTTGCCATGGCCCTCGCCC 507

Qy 529 GTGCTCGCCCTGCACCGCTGTTCACCGGCGCGCGCG-----CCTACTGCAGTGAG 579

Db 508 GTGGCTTACCAACGAGGCTCTTCCACCGCGCGCAGCAACAGACCTTCTGCTGGGAG 567

Qy 580 GCCTTCCCGAGCGCGCGCTGGAGCGCGCTTGGCACTGTACACCTGCTGGCGCTGTAC 639

Db 568 CAGTGGCGCGACCTCGCCACAAAGAGGCTTACGTTGGTGTGCACCTTCTGCTTCCGCTAC 627

Qy 640 CTGCTGCGCGTGTGCGCACCTGCGCTGTATGCGGCCCATGTGCGGCCACTG 693

Db 628 CTGCTGCGCGTCTGCTGCTCATCTGCTTCTGTATGCCAAGTCTCTTAATCACTTG 681

RESULT 15

US-09-826-509-502

; Sequence 502, Application US/09826509

; Patent No. 8806054

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinema, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

CURRENT APPLICATION NUMBER: US/09/826,509

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 60/195,747

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 589

SOFTWARE: PatentIn Version 2.1

SEQ ID NO 502

LENGTH: 1050

TYPE: DNA

ORGANISM: Homo sapiens

US-09-826-509-502

Query Match 14.3%; Score 171.2; DB 3; Length 1050;

Best Local Similarity 58.2%; Pred. No. 9.9e-19;

Matches 346; Conservative 0; Mismatches 233; Indels 15; Gaps 2;

Qy 115 GCGGTGAGCGCTGGCTCGTGGCGCTCTTCTTTCGCGCGCTGATGCTGCGGCTGGT 174

Db 88 GCGGTGAGAACTTCTGTCACCGTGGTGTGTTTGGCGCTGATCTTTCGCGCTGGGCTGCTG 147

Qy 175 GGGAACTCGCTGGTCTAGCTATCTGCGGCCACAAAGCCGAT-----CGGACCGGTG 228

Db 148 GGCACACCTTAGTATCACCGTGTGGCGGCGACGAGCCGGGAGCCGCGGAGCACC 207

Qy 229 ACCAACTTCTATGCGCAACCTGCGGCGCCAGGACGTGACCTTCTCTGCTGCTGCTC 288

Db 208 ACCAACTTCTATGCGCAACCTGCGGCGCCAGGACGTGACCTTCTCTGCTGCTC 267

Qy 289 CCCTTACGCGCCCTGCTGTATCCCGCTGCCCGGCTGGGTGTGGGGGAGCTTCTCATGTGCAAG 348

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
i
OM nucleic - nucleic search, using sw model
Run on: February 15, 2006, 02:17:31 ; Search time 5400 Seconds
(without alignments)
10371.137 Million cell updates/sec
Title: US-10-771-417-6
Perfect score: 1197
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc:*
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6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
1	1195.4	99.9	1582	4	CR621438	CR621438 full-length
2	830.4	69.4	3075	4	AK039628	Mus muscu
C 3	627.6	52.4	1032	1	AL568705	AL568705
4	593.4	49.6	872	1	AL541044	AL541044
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6	347.6	29.0	600	7	CK623581	milli03.y
7	279.6	23.4	650	1	BB193083	BB193083
8	277.6	23.2	759	8	DN693330	AGENCOURT
C 9	275.8	23.0	591	7	CO039966	UI-M-BH3-
10	246.2	20.6	465	7	CN367647	CO039966
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15	195.8	16.4	960	6	CA487873	BE309856
16	186.2	15.6	1164	11	DO051286	AGENCOURT
C 17	174	14.5	448	2	BE949364	DO051286
18	173.4	14.5	1257	10	AY400332	Homo sap
C 19	173.2	14.5	454	1	AI823800	BE949364
20	169.8	14.2	721	6	CF147813	UI-M-BH3-
21	166.4	13.9	1287	10	AY400334	AI823800
22	161	13.5	815	9	BZ197821	wj14h01.x

C	23	157.6	13.2	363	9	AZ981549	AZ981549
C	24	157	13.1	387	6	CA432866	CA432866
C	25	156.2	13.0	460	1	AI819198	AI819198
C	26	155	12.9	730	6	CF147825	CF147825
C	27	154.2	12.9	441	5	BY260374	BY260374
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	32	138.6	11.6	668	7	CO918721	CO918721
	33	136	11.4	136	11	DQ046674	DQ046674
	34	135.6	11.3	898	10	AY400987	AY400987
	35	134.8	11.3	1918	4	AK053776	AK053776
	36	132.6	11.1	800	10	AY409238	AY409238
	37	131.6	11.0	1095	10	AY400986	AY400986
	38	129	10.8	468	5	BX281894	BX281894
	39	128.6	10.7	849	10	AY409237	AY409237
	40	122.2	10.2	937	11	CNS03GSG	AL2433385
	41	121	10.1	1113	10	AY420480	AY420480
	42	120.4	10.1	1119	11	DQ035375	DQ035375
	43	115.4	9.6	1100	10	AY420481	AY420481
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	45	111.8	9.3	899	7	CN838037	CN838037

ALIGNMENTS

RESULT 1
CR621438
LOCUS full-length cDNA clone CS0DE005YCI17 of Placenta of Homo sapiens
DEFINITION (human)
ACCESSION CR621438.1 GI:50502245
VERSION HTC; CNSLT cDNA.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1582)
AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1582)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
Location/Qualifiers
1. 1582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE005YCI17"
/tissue type="Placenta"
/plasmid="pCMVSPORT_6"

Query Match 99.9%; Score 1195.4; DB 4; Length 1582;
Best Local Similarity 99.9%; Pred. No. 1.1e-206;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCACACCGCTGCTACGTCGGACCCCAACGGCTCCTCGGGGGCACCGGCCAACGCGCTCC 60
Db |||||
161 ATGCACACCGTGGCTACGTCGGACCCCAACGGCTCCTCGGGGGCACCGGCCAACGCGCTCC 220
Qy 61 GCGTCCCGGGGTGTGGGCGCCAAACGCTTCGACAGCGCCAGTCCCTTCGCCCGCGGGCCGTG 120
Db |||||
221 GCGTCCCGGGGTGTGGGCGCCAAACGCTTCGACAGCGCCAGTCCCTTCGCCCGCGGGCCGTG 280
Qy 121 GACGCTCGGCTCGTCCGCTCTCTTCGCGCGCGCTGATGCTGCTGGGCTCGTGGGGGAAC 180
Db |||||
281 GACGCTCGGCTCGTCCGCTCTCTTCGCGCGCGCTGATGCTGCTGGGCTCGTGGGGGAAC 340
Qy 181 TCGCTGGTCACTACGTCATCTGCGCGCCACAGCGGATCGGACCGTGCACCACTTCTAC 240
Db |||||
341 TCGCTGGTCACTACGTCATCTGCGCGCCACAGCGGATCGGACCGTGCACCACTTCTAC 400
Qy 241 ATCGCCAAACCTGGCGGCCACGACGCTGACCTTCCTGCTGCTGCTGCCCTTCACGGCC 300
Db |||||
401 ATCGCCAAACCTGGCGGCCACGACGCTGACCTTCCTGCTGCTGCTGCCCTTCACGGCC 460
Qy 301 CTGCTGTACCGCTGCGCGCTGCGGTGCTGGGCGACTTCATGTGAAGTTTCGTCACACTAC 360
Db |||||
461 CTGCTGTACCGCTGCGCGCTGCGGTGCTGGGCGACTTCATGTGAAGTTTCGTCACACTAC 520
Qy 361 ATCCAGCAGGCTCGGTGACGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db |||||
521 ATCCAGCAGGCTCGGTGACGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 580
Qy 421 TGGTACGTCAGGCTGCTCCGCTGCGCGCTGCGACCGCCGCTGCGCGCTGCGCGCTG 480
Db |||||
581 TGGTACGTCAGGCTGCTCCGCTGCGCGCTGCGACCGCCGCTGCGCGCTGCGCGCTG 640
Qy 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGCGGCTGTCTGCGCGGCTGCTGCGCGCTG 540
Db |||||
641 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGCGGCTGTCTGCGCGGCTGCTGCGCGCTG 700
Qy 541 CACGCGCTGTCACCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db |||||
701 CACGCGCTGTCACCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 760
Qy 601 GAGCGCGCTTTCGCACTGTACAACTGCTGCGCGCTGTACCTGCTGCTGCTGCTGCTGCTGCTG 660
Db |||||
761 GAGCGCGCTTTCGCACTGTACAACTGCTGCGCGCTGTACCTGCTGCTGCTGCTGCTGCTGCTG 820
Qy 661 TCGCGCTGCTATGCGGCCATGCTGCGCCACTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 720
Db |||||
821 TCGCGCTGCTATGCGGCCATGCTGCGCCACTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 880
Qy 721 GCGGATAGCGCCCTGCAGGGCAGGTGCTGCGCAGCGCGCGCGCGCTGCGGGGCCAAG 780
Db |||||
881 GCGGATAGCGCCCTGCAGGGCAGGTGCTGCGCAGCGCGCGCGCGCTGCGGGGCCAAG 940
Qy 781 GTCTCGCGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db |||||
941 GTCTCGCGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1000
Qy 841 CTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db |||||
1001 CTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1060
Qy 901 GCCTACGCGCTTACAGCTGGGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db |||||
1061 GCCTACGCGCTTACAGCTGGGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120
Qy 961 CTGCTCTACGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db |||||
1121 CTGCTCTACGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1180
Qy 1021 GCG 1080
Db |||||
1181 GCG 1240
Qy 1081 GCGGAGCTGCACCGCTCGGGTCCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140

Db 1241 GCGGAGCTGCTCCGCCCTGGGGTCCACCCGCCCCCGCAGGGCGCAGAGCCAGGGAGC 1300
Qy 1141 AGTGGGCTGGCGCGCGCGCGCTGTGGCTCTGGGGGAGGACAAACGCCCTCTCTGA 1197
Db 1301 AGTGGGCTGGCGCGCGCGCGCTGTGGCTCTGGGGGAGGACAAACGCCCTCTCTGA 1357

RESULT 2
AK039628 3075 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus adult male spinal cord cDNA, RIKEN full-length
DEFINITION enriched library, clone:A330075J02 product:G-PROTEIN-COUPLED
RECEPTOR GPR54 (G PROTEIN-COUPLED RECEPTOR 54), full insert
sequence.
ACCESSION AK039628
VERSION AK039628.1 GI:26333372
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2
3 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
4
5 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
6
7 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
8
9 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
10 (bases 1 to 3075)
11 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuura, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohashi, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Shiraki, T.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URU: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URU: <http://genome.gsc.riken.jp/>
URU: <http://fantom.gsc.riken.jp/>

FEATURES

Source

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1. .3075
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/dev stage="adult"
1705' .2895
/note="unnamed protein product;
GPR54 (G PROTEIN-COUPLED RECEPT
evidence: FASTA, 100%ID, 100%le
putative"

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CDS

ORIGIN

Query Match	69.4%;	Score 830.4;	DB 4;	Length 3075;
Best Local Similarity	82.2%;	Pred. No. 1.5e-140;		
Matches 954;	Conservative 0;	Mismatches 206;	Indels 0;	Gaps 0;
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1705	ATGGCCACCGAGGGACATTGGCTCCCAATGTGACCTGGTGGGTCCGTCCAAAGCTTCA	1764		
61	GGCTGCCCGGGCTGTGGGCGCAACGCCCTCGACGCGCCAGTCCCTTGGCCGGGGCCGTG	120		
y				
1765	GGATGCCACGAGGTGGGGTGTCAACGCCCTCGGATGACCCAGGCTCTGGCCAAAGGCCCTG	1824		
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121	GACGCTGGCTCGTGGCCGCTCTTCTTGGGGGGCTGATGCTCTGGGGCTGGTGGGAAC	180		
y				
1825	GATGCTGGCTGGTTCCTCCCTGTTTTTCGCTACACTCATGTTGCTGGGCTGGTCCGAAC	1884		
b				
181	TCGCTGGTTCATCTACGTGTCATCTGCCGCCACAGCCGATGCGGACCGGTGACCAACTTCTAC	240		
y				
1885	TCATTGGTTCATCTACGTTCATCTGCCGCCACAGCACATGACAGACAGTTACCAACTTCTAC	1944		
b				
241	ATCGCCAACTGGCGGCCACGAGACGTGACCTTCCTCTGTGCTGGCTCCCTTCCACGGCC	300		
y				
1945	ATCGCTAACCTGGCTGCCACAGACGTCATTTCTTACTGTGCTGGTGGCCCTTCCACGCA	2004		
b				
301	CTGCTGTACCCGCTGCCCGGCTGGGTGCTGGGGCGCACTTCATGTGCAAGTTGCTCAACTAC	360		
y				
2005	CTTCCTTACCCGCTGCCCGGCTGGGTGCTGGGAGACTTCATGTGCATAATTCGTCAACTAC	2064		
b				
361	ATCCAGCAGGCTCTGGGTGACGAGCCACGCTGTGCCACTCTTGACCGGCCCATGAGTGTGGACCGC	420		

COMMENT On Feb 16, 2001 this sequence version replaced gi:30604434.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 9538.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE005AB09NP1&c=9538.f.

FEATURES
source
Location/Qualifiers
1..1032
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE005YC17"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 52.4%; Score 627.6; DB 1; Length 1032;
Best Local Similarity 92.1%; Pred. No. 9e-104;
Matches 691; Conservative 20; Mismatches 34; Indels 5; Gaps 5;
QY 448 GCCCTGCACCGCCGACGCGCCCTGCGGTGTCAGCCTCAGATCTGGTAGGC 507
DB 970 GCGCCCTGMAACCGGMAACCGCCCTGSGGTGCTTTTCAS-CTSMGATCTGGGTARG- 913
QY 508 TCTGGGGGGTGTCTGCGCGGTGTCGCCCTGACACCGCCTGTACCGGGCCGCGGCC 567
DB 912 TTTGGCGGCGT-TTTGGCGGCGTGTCTKSCCTGACACCGCTTGTACCGGGCCGCGGCC 854
QY 568 TACTGCAGTAGGCGCTTCCACGACGCGCCCTTGAGCGCGCTTTCGCACTGTACAACTG 627
DB 853 WACTGCATAGGCGCTTCCCGACGCGCGCCCTGGRGCGCGCTTTCGCACTGTACACCT 794
QY 628 CTGGCGCTGTACTGCTGCGCGTGTCTGCGACCTGCTGCTGTATGCGGCGATGCTGCGC 687
DB 793 STGGCGCTGTACTGCTGCGCGTGTCTGCGACCTGCGCTGTATGCGGCGCATGTGCGC 734
QY 688 CACCTGGGCGGTGCTGCG 747
DB 733 CACCTGGGCGCTGCTGCG 674
QY 748 CTGGCAGAGCGCGCAGGCG 807
DB 673 CTGGCAGAGCGCGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 614
QY 808 CTGCTCTTTCGCGCGCTGCTGGGGCCCCATTCAGTGTTCCTGGTGTCTGACGCGCTGGC 867
DB 613 CTGCTCTTTCGCGCGCTGCTGGGGCCCCATTCAGTGTTCCTGGTGTCTGACGCGCTGGC 554
QY 868 CCGCGGGGCTCTGCGACCGCAGCTACGCGCGCTACGCGCTTAAGACCTGGGCTCAC 927
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QY 928 TGCATGTCTTACAGAACTCCGCGCTGAACCGCGCTGTCTAGCGCTTCTGGGCTCGCAC 987
DB 494 TGCATGTCTTACAGAACTCCGCGCTGAACCGCGCTGTCTAGCGCTTCTTGTAGCTCGCAC 435
QY 988 TTCCGACAGGCGCTTCCGCGCGGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1047
DB 434 TTCCGACAGGCGCTTCCGCGCGGTCTGCGCGCT-CGCGCGCGCGCGCGCGCGCGCGCG 376
QY 1048 CGGCGCGGACCTCGGACCGCGCAGCCCCACACGCGGAGCTGCACCGCTGGGGTCCAC 1107

Db 375 CRGCCCCRACCTCGGACCCCGGACCCCAACACCGGAGCTGCACCCCTGGGTCCAC 316
QY 1108 CCGCCCCCCCCCAGGCGCGAGAACCCAGGAGCAGTGGCTGGCGCGCGCGGCTGTGC 1167
Db 315 CCGCCCCCCCCCAGGCGCGAGAACCCAGGAGCAGTGGCTGGCGCGCGCGGCTGTGC 256
QY 1168 GTCTGGGGGAGGACACGCGCCCTCTCTGA 1197
Db 255 GTCTGGGGGAGGACACGCGCCCTCTCTGA 226

RESULT 4
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LOCUS
DEFINITION AL541044 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE005YC17
5-PRIME, mRNA sequence.
ACCESSION AL541044
VERSION AL541044.3 GI:45716638
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 872)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30544835.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 9538.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE005AB09QP1&c=9538.f.

FEATURES
source
Location/Qualifiers
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 49.6%; Score 593.4; DB 1; Length 872;
Best Local Similarity 91.6%; Pred. No. 1.4e-97;
Matches 655; Conservative 15; Mismatches 37; Indels 8; Gaps 4;
QY 1 ATGCACACCGTGGGTAGTCCGGACCCCAACGCGCTCTGGGGGACCGGCAACGCGCTCC 60
DB 159 ATGCACACCGTGGGTAGTCCGGACCCCAACGCGCTCTGGGGGACCGGCAACGCGCTCC 218
QY 61 GGCTGCCCGGCTGTGGCGCCCAACGCGCTCGGACGCGCCAGTCCCTTGGCCGCGGCGGTG 120
DB 219 GGCTGCCCGGCTGTGGCGCCCAACGCGCTCGGACGCGCCAGTCCCTTGGCCGCGGCGGTG 278
QY 121 GACGCGCTGGTCTGCGCGCTTCTTCTTCTGCGCGCTGTATGCTGTGCGGCTGGTGGGAAC 180
DB 279 GACGCGCTGGTCTGCGCGCTTCTTCTTCTGCGCGCTGTATGCTGTGCGGCTGGTGGGAAC 338

[illegible]

RESULT 9
 CO039966/c
 LOCUS
 CO039966
 591 bp mRNA linear EST 10-JUN-2004
 DEFINITION
 UI-M-BH3-avi-a-09-0-UI.s1 NIH BMAP_M_S4 Mus musculus cDNA clone
 UI-M-BH3-avi-a-09-0-UI 3' mRNA sequence.

FEATURES
SOURCE

RESULT 10	
CN367647	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
PUBMED	
COMMENT	
FEATURES	

into DH10B bacteria (Life Technologies) to generate the NIH-SNAPTM S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996).
TAG: SEO=None found"

ORIGIN

Query Match	23.0%;	Score 275.8;	DB 7;	Length 591;
Best Local Similarity	78.3%;	Pred. No. 5.4e-40;		
Matches 331;	Conservative 0;	Mismatches 92;	Indels 0;	Gaps 0;
Qy	738	GGGGCAGGTGCTGGCAGAGCGCGCAGCGCGCTGCGGGGCCAAGGTCCTCGCGGCTGCTGGC	797	
Db	576	GGGACAGCTGCTAGCACACGGCGCGGAGCAGTGCACACCAAGTCTCCCGGCTGGTGGC	517	
Qy	798	GGCCGTGTCCTGCTCTTTCGCGCGCTGCTGGGGCCCCATCCAGACTGTTCTTGCTGTGTCGA	857	
Db	516	CGTGTGCTGCTGCTCTTTCGCGCGCTGCTGGGGCCCGATCCAGACTGTTCTTGCTGTGTTCA	457	
Qy	858	GGCGCTGGGCCCCCGGGGCTCTTGGCACCCACACAGCTACGCCGCTACGCGCTTAAGAC	917	
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Qy	978	GGGCTCGCACTTCCGACAGGCTTCCGCGCGCTGCTGCCCTGGCGCGCGCGCGCCCCG	1037	
Db	336	GGTTTCACATTCAGACAGGCTTCTGCGCGCTGTGCCCTGCTGCGGCAAGCCAGCG	277	
Qy	1038	CGCCCCCGCGCGCCCGGACCTCTGGACCCCGCAGCCCCACACGCGGAGTGTCACCGCCT	1097	
Db	276	CGGGCCCCACACTGACGCGCACTCGGACCGAGTGTGCAACTCACACTGTGCGGCACAGCCG	217	
Qy	1098	GGGGTCCCAACCGGGCCCCCGCAGGCGCAGAAAGCCAGGAGGACAGTGGGTGTCGCCCGG	1157	
Db	216	TGCTGGCAACCTGTGCGGATCAGGAGCCGCGAGCTTGGGAACCTGTGGTGGCTGCGCC	157	
Qy	1158	CGG 1160		
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RESULT 10	
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LOCUS	465 bp mRNA linear EST 16-MAY-2004
DEFINITION	170005312190525 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION	CN367647
VERSION	CN367647.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 465)
AUTHORS	Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
TITLE	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED	15146197
COMMENT	Contact: Brandenberger R Regenerative Medicine Genon Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@genon.com Insert Length: 465 Std Error: 0.00.
FEATURES	Location/Qualifiers

source	1. .465 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /tissue_type="embryonic stem cells, cell lines H1, H7, and H9" /clone_lib="GRN_ES" /note="oligo dt primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"
source	1. .507 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="RZPDp9016C2132" /tissue_type="T-Lymphocytes" /lab_host="DH10B" /clone_lib="RZPD no.9016" /note="Vector: pQE80LSN_cloned; Site_1: SalI; Site_2: NotI; vector: http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml ; 1st strand cDNA was prepared from mRNA obtained from human T-Lymphocytes with a NotI - oligo(dt) primer [5', GACTAGTCTAGATCGGAGCGCGCCCTTTTCTTTT 3'] Double-stranded cDNA was ligated to SalI adaptors, digested with NotI and cloned into the NotI and SalI sites of the pQE80LSN_cloned vector"
ORIGIN	
Query Match	20.6%; Score 246.2; DB 7; Length 465;
Best Local Similarity	90.4%; Pred. No. 1.3e-34;
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QY	1 ATGCACACCGTGGCTACGTCGGACCCAAACGCTCGGACGGCTCTGGGGGGCACCGGCCCAACGCCTCC 60
Db	94 ATGCACACCGTGGCTACGTCGGACCCAAACGCTCTGGGGGGCACCGGCCCAACGCCTCC 153
QY	61 GGCTGCCCGGCTGTGGCGCCAAACGCTCGGACGGCTCTGGCGCGGGCCGCTG 120
Db	154 GGCTGCCCGGCTGTGGCGCCAAACGCTCGGACGGCTCTGGCGCGGGCCGCTG 213
QY	121 GACGCTGGCTGTGGCGGCTCTTTCTTGGCGGCGTGATGCTGCTGGGCTGTGTGGGAAC 180
Db	214 GACGCTGGCTGTGGCGGCTCTTTCTTGGCGGCGTGATGCTGCTGGGCTGTGTGGGAAC 273
QY	181 TCGTGGTCACTAGTCATCTGCGCCACAGCCGATGCGGACCGTGACCAACTTCTAC 240
Db	274 TCGTGGTCACTAGTCATCTGCGCCACAGCCGATGCGGACCGTGACCAACTTCTAC 333
QY	241 ATTCGCCAACCTGGCGGCGTGCAGCTGACCTTCCTCTCTGTGTGGTCTCCC 291
Db	334 ATCGGTGAGTGGCGGCTGCGCCAGCCTGCTGCGCTCCGGGGGCTCC 384
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DEFINITION	
ACCESSION	CR982913
VERSION	CR982913.1 GI:68221247
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	
AUTHORS	Heil, O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D. and Korn, B.
TITLE	Human T-Lymphocytes library
JOURNAL	Unpublished (2005)
COMMENT	Contact: Inge Arlt RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Email: www.rzpd.de RZPD; RZPDp9016C2132. RZPDLib; (Human T-Lymphocytes) RZPD LIB No.9016 http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact: Inge Arlt RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 100 Fax: +49 30 32639 111 www.rzpd.de This clone is available from RZPD: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPDp9016C2132 contact RZPD (product- support@rzpd.de) for further information. Primer name: qe3_4 , Primer sequence: CGATAACCAATTACACAG.
FEATURES	Location/Qualifiers
ORIGIN	
Query Match	20.4%; Score 244; DB 7; Length 507;
Best Local Similarity	100.0%; Pred. No. 3.2e-34;
Matches	244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGCACACCGTGGCTACGTCGGACCCCAACGCTCTCTGGGGGGCACCGGCCCAACGCCTCC 60
Db	217 ATGCACACCGTGGCTACGTCGGACCCCAACGCTCTCTGGGGGGCACCGGCCCAACGCCTCC 276
QY	61 GGCTGCCCGGCTGTGGCGCCAAACGCTCGGACGGCTCTGGCGCGGGCCGCTG 120
Db	277 GGCTGCCCGGCTGTGGCGCCAAACGCTCTCGGACGGCTCTCTGGCGCGGGCCGCTG 336
QY	121 GACGCTGGCTGTGGCGGCTCTTTCTTGGCGGCGTGATGCTGCTGGGCTGTGTGGGAAC 180
Db	337 GACGCTGGCTGTGGCGGCTCTTTCTTGGCGGCGTGATGCTGCTGGGCTGTGTGGGAAC 396
QY	181 TCGTGGTCACTAGTCATCTGCGCCACAGCCGATGCGGACCGTGACCAACTTCTAC 240
Db	397 TCGTGGTCACTAGTCATCTGCGCCACAGCCGATGCGGACCGTGACCAACTTCTAC 456
QY	241 ATCG 244
Db	457 ATCG 460
RESULT 12	
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DEFINITION	
ACCESSION	CR9844117
VERSION	CR9844117.1 GI:19427702
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE	
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
TITLE	NIH-MGC
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Straubeberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Dr. James Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov This clone was contributed by the Brain Molecular Anatomy Project (BMAP)


```

601093479F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:348082 5',
mRNA sequence.
ACCESSION BE309856
VERSION BE309856.1 GI:9168690
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

DEFINITION
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 671)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM8526 row: n column: 19
High quality sequence stop: 420.
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1. .671
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    /mol_type="mRNA"
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    /tissue_type="tumor, gross tissue"
    /dev_stage="7 months"
    /lab_host="DH10B"
    /clone_lib="NCI CGAP Mams"
    /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
    Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
    Library constructed by Life Technologies. Investigators
    providing samples: Lothar Hennighausen/Robin Humphreys,
    NIH"

ORIGIN
Query Match 16.6%; Score 198.6; DB 2; Length 671;
Best Local Similarity 69.2%; Pred. No. 5.3e-26;
Matches 330; Conservative 0; Mismatches 139; Indels 8; Gaps 4;

QY 1 ATGCACACCGTGCTACGTCCGAGACCAACGCGTCTCTGGGGGCGACCGGCCAACCGCTCC 60
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Db 127 ATGGCCACCGAGCGGACATGGCTCCCAATGTGACCTGGTGGGCTCCGTCCAAACGTTCA 186
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QY 61 GGCTGCCCGGGCTGTGGCGCCCAACGCTCGGAGCGGCCAGTCCCTTCGCGCGGCGCGTG 120
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Db 187 GGATGCCCAAGGTGCGGTGTCAACGCTCGGATGACCCAGGCTCTCGCGCAAGGCCCTG 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 GAGCGCTGCTGTCGCGCTCTTTCTTCGCGCGCTGATGCTCTGGCGCTGTGGGGAC 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 247 GATGCTTGCTGTTCCCTGTTTTCGCTACACTCATGTTGCTTGGGCTGTGCGGAAC 306
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QY 181 TCGTGGTTCATCTACGTCACTCTCGGCCACAAGCCGATCGGACCGTGCACCAAC-TTCTA 239
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QY 359 ACATCC---AGCAGGTCTCGGTGCAGGCCACCGTGTG---CCACTCTGACCGCCATGAGTG 412
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Db 487 TCATCCCGCCAGGTTCTCCGGTGCAGGCACATGTGTCCACTCTGTACGGGGCTTAGTGT 546
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RESULT 15
CA487873
LOCUS CA487873
DEFINITION AGENCOURT_10811154 MAPcL Homo sapiens cDNA clone IMAGE:6719495 5',
mRNA sequence.
ACCESSION CA487873
VERSION CA487873.1 GI:24948297
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 960)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM14277 row: h column: 23
High quality sequence start: 40
High quality sequence stop: 488.
FEATURES
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1. 960
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    /mol_type="mRNA"
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    /lab_host="EMDH10B"
    /clone_lib="MAPcL"
    /note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
    Subtracted with brain, liver, lung, kidney and muscle.
    Directionally cloned. Priming method: oligo-dt. Average
    insert size: 1800 bp. Library amplification: 26,000 fold.
    Kristi A. Eglund, James J. Vincent, Robert Strausberg,
    Bungkok Lee & Ira Pastan: Discovery of new breast
    cancer genes encoding membrane and secreted proteins.
    Manuscript submitted."

ORIGIN
Query Match 16.4%; Score 195.8; DB 6; Length 960;
Best Local Similarity 88.7%; Pred. No. 1.7e-25;
Matches 212; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Db 355 GGTCTTATCTCTGGTTGTGCACAGGCTCTGCGCGGTGTCTGCGCGGTGTCTGCGCT 414
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QY 540 GCACCGCTGTACCCCGGCGCGCCTACTGCAGTAGGCGCTTCCCGAGCGCGCCT 599
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Db 415 GCACCGCTGTACCCCGGCGCGCCTACTGCAGTAGGCGCTTCCCGAGCGCGCCT 474
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QY 600 GGAGCGCGCTTCGACTGTACAACCTGCTGGCGCTGTACCTGTGCGCTGTCTGCCAC 659
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Db 475 GGAGCGCGCTTCGACTGTACAACCTGCTGGCGCTGTACCTGTGATGACGCTGTGCCAC 534
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QY 660 CTGCGCTGTATGCGGCCATGCTGCGCCACCTGCGCGGGTCTGCGCGCGCGCGCGC 718
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Db 535 CTGCGCCTGCTATGCGGCCATGCTGCCCCACCTGGGCCCGGGTCCGCTCCGCCCCCCCCC 593

Search completed: February 15, 2006, 06:06:48
Job time : 5405 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 01:15:56 ; Search time 810 Seconds

(without alignments)
9848.935 Million cell updates/sec

Title: US-10-771-417-6

Perfect score: 1197

Sequence: 1 atgcacacgtggtacgtc.....aggacaacgcccctctctga 1197

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*
- 14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1197	100.0	1197	3	AAA39343
2	1197	100.0	1197	4	AD07921
3	1197	100.0	1197	8	AB242844
4	1197	100.0	1197	11	ADN39429
5	1197	100.0	1197	11	ADN39504
6	1197	100.0	1197	12	ADL1584
7	1197	100.0	1197	12	ADO2925
8	1197	100.0	1197	14	ACL38952
9	1197	100.0	1197	14	ADZ68968
10	1195.4	99.9	1197	3	AAA64352
11	1195.4	99.9	1197	4	AHA49533
12	1195.4	99.9	1197	8	ABX95717
13	1195.4	99.9	1197	9	ACA62277
14	1195.4	99.9	1197	12	ADG19756
15	1195.4	99.9	1197	13	ADS88806
16	1195.4	99.9	1197	13	ADU61174
17	1195.4	99.9	1609	4	AA514575
18	1195.4	99.9	1609	12	ADG19754
19	1195.4	99.9	1609	13	ADQ89079

20	1195.4	99.9	1617	8	ACC49540
21	1195	99.8	1197	6	ABQ81125
22	1194	99.7	1194	13	ADR21326
23	1194	99.7	1194	13	ADT05942
24	1192.2	99.6	1197	4	AD08840
25	1179.4	98.5	1194	4	AD07922
26	906.4	75.7	969	10	ADC12677
27	836.4	69.9	1188	13	ADR21328
28	836.4	69.9	1188	13	ADT05944
29	836.4	69.9	1191	3	AAA39340
30	836.4	69.9	1191	6	AB558354
31	836.4	69.9	1237	8	ABX95718
32	836.4	69.9	1237	9	ACA62278
33	832	69.5	1188	4	AAI66036
34	832	69.5	1188	6	AB554395
35	832	69.5	1188	13	ADR21330
36	832	69.5	1188	13	ADT05946
37	832	69.5	1191	6	ABQ81126
38	832	69.5	1191	12	ADO30215
39	808.8	67.6	1254	3	AAA64353
40	245	20.5	548	4	AA30775
41	186.8	15.6	1309	8	ABZ42788
42	186.8	15.6	1309	14	ADX25933
43	186.8	15.6	1365	2	AAT79976
44	186.8	15.6	1365	9	ADA09963
45	186.8	15.6	1365	11	ADL80089

ALIGNMENTS

RESULT 1

AAA39343

ID AAA39343 standard; cDNA; 1197 BP.

XX AAA39343;

DT 11-SEP-2000 (first entry)

DE Human G protein-coupled receptor protein hOT7T175 encoding cDNA.

XX G protein-coupled receptor protein; rOT7T175; hOT7T175; tumour;

KW guanine nucleotide binding protein; cytosolic; anti-proliferative;

KW cancer; diagnosis; ss.

OS Homo sapiens.

XX WO200024890-A1.

PN 04-MAY-2000.

PF 26-OCT-1999; 99WO-JP005905.

PR 27-OCT-1998; 98JP-00305949.

PR 04-FEB-1999; 99JP-00027710.

PR 04-MAR-1999; 99JP-00057207.

XX 29-SEP-1999; 99JP-00276225.

PA (TAKE) TAKEDA CHEM IND LTD.

XX Watanabe T, Terao Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;

XX WPI; 2000-350732/30.

DR P-PSDB; AA91094.

XX G protein coupled receptor protein, antibodies to it and a method of

PT screening compounds which alter the binding of the receptor to its

PT ligands for treatment of diseases including tumors.

XX Claim 6; Page 105-106; 11app; Japanese.

PS The present sequence encodes a human G protein-coupled receptor protein

XX designated hOT7T175. The G protein-coupled receptor protein has

CC

polynucleotide are useful for treating and diagnosing infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by human immunodeficiency virus (HIV)-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting, dyskinesias, sleep disorders, psychotic and neurological disorders including anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation. AXOR12 protein and polynucleotide are also useful for screening and structure based designing of antagonists, agonists and inhibitors of AXOR12. The protein is useful in screening assays and to identify membrane bound or soluble receptors. The polynucleotide is useful for chromosome localisation studies, as diagnostic reagents for detecting mutations in associated genes, recombinant production of AXOR12 protein, as valuable tools for tissue expression studies and in gene therapy. AXOR12 protein and polynucleotide are also useful as vaccines

Sequence 1197 BP; 131 A; 481 C; 385 G; 200 T; 0 U; 0 Other;

Query Match 100.0%; Score 1197; DB 4; Length 1197;
Best Local Similarity 100.0%; Pred. No. 2.2e-167;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCACACCGTGGCTACGTCCGGACCCCAACGCGTCTCTGGGGGGCAACCGGCCCAACGCTCC 60
Db 1 ATGCACACCGTGGCTACGTCCGGACCCCAACGCGTCTCTGGGGGGCAACCGGCCCAACGCTCC 60
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Db 241 ATGCGCAACCTGGCGGCCGACGAGCTGACCTTCCTCTGCTGTGCGTCCCTTCACGCGC 300
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Db 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGGGGGGGTGTCTGCGCGGTGCTGCGCTG 540
Qy 541 CACCGCTGTACCGCGGGCGCGCTACTGCACTGAGGCGCTTCCCGACGCGCGCCCTG 600
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Qy 601 GAGCGCGCTTCGCACTGCACTGCAAACTGTGGCGCTGTACTCTGCTGCGCGCTGCTGCGCACC 660
Db 601 GAGCGCGCTTCGCACTGCACTGCAAACTGTGGCGCTGTACTCTGCTGCGCGCTGCTGCGCACC 660
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Qy 721 GCCGATAGCGCCCTGACAGGGGACAGTCTGTGCAGAGCGCGCAGCGCGCGTCTCGGGCCAAAG 780
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Qy 781 GTCTCGCGGCTGTGGGGCGCGTGGTCTCTTCCGCGCTCTTGGGGGGCCCATCCAG 840
Db 781 GTCTCGCGGCTGTGGGGCGCGTGGTCTCTTCCGCGCTCTTGGGGGGCCCATCCAG 840
Qy 841 CTGTCTCTGTGTGCTGCAAGGCGCTGGGCGCCCGCGGGCTCTTGGCACCCCAACGAGCTACGCC 900
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Qy 1141 AGTGGGCTGGCG 1197
Db 1141 AGTGGGCTGGCG 1197
RESULT 3
ABZ42844
ID ABZ42844 standard; DNA; 1197 BP.
XX AC ABZ42844;
XX DT 04-MAR-2003 (first entry)
XX DE Human G protein-coupled receptor GPR54 nucleotide SEQ ID NO:476.
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX KW ulcer; gene; ds.
OS Homo sapiens.
XX WO200261087-A2.
XX PN 08-AUG-2002.
XX PD 19-DEC-2001; 2001WO-US050107.
XX PF 19-DEC-2000; 2000US-0257144P.
XX PR (LIFE-) LIFESPAN BIOSCIENCES INC.
XX PA Burmer GC, Roush CL, Brown JP;
XX PI WPI; 2003-046718/04.
XX DR P-PSDB; ABP81995.
XX PT New isolated antigenic peptides e.g., for G protein-coupled receptors

PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.

PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP1675 to ABP82018, which are used in the
CC exemplification of the present invention

XX SQ Sequence 1197 BP; 131 A; 481 C; 385 G; 200 T; 0 U; 0 Other;

Query Match		100.0%;	Score 1197;	DB 8;	Length 1197;
Best Local Similarity		100.0%;	Pred. No. 2.2e-167;		
Matches 1197;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCACACCGTGGCTACCTCGGACCCCAACGCGTCTCGGGGGGACCGGGCAACGCGCTCC	60		
DB	1	ATGCACACCGTGGCTACCTCGGACCCCAACGCGTCTCGGGGGGACCGGGCAACGCGCTCC	60		
QY	61	GGCTCCCGGGCTGGGGCCCAAGCCCTCGGACGGCCAGTCCCTTCGCGCGGGCGGTG	120		
DB	61	GGCTCCCGGGCTGGGGCCCAAGCCCTCGGACGGCCAGTCCCTTCGCGCGGGCGGTG	120		
QY	121	GACGCTGGCTGTCGCGCGCTCTTCTTCGCGGGCTGTGCTGCTGGGCTGTGGGGAAC	180		
DB	121	GACGCTGGCTGTCGCGCGCTCTTCTTCGCGGGCTGTGCTGCTGGGCTGTGGGGAAC	180		
QY	181	TGCTGTGTCATCTAGTCATCTGCGCGCCCAAGCCGATGCGGACCGGTGACCACTTCTAC	240		
DB	181	TGCTGTGTCATCTAGTCATCTGCGCGCCCAAGCCGATGCGGACCGGTGACCACTTCTAC	240		
QY	241	ATCGCCACCTGGGGCCGACGAGTACCTTCCTCGGCGGCTGCTGCTGCTGCTGCTGCTG	300		
DB	241	ATCGCCACCTGGGGCCGACGAGTACCTTCCTCGGCGGCTGCTGCTGCTGCTGCTGCTG	300		
QY	301	CTGCTGTACCGGCTGCGCGGCTGGGTGCTGGGCGACTTTCATGTGCAAGTTCGTCAACTAC	360		
DB	301	CTGCTGTACCGGCTGCGCGGCTGGGTGCTGGGCGACTTTCATGTGCAAGTTCGTCAACTAC	360		
QY	361	ATCAGCAGGTCTCGGTGACGCGCACGTGTGCACTCTGACCGGCATGAGTGTGACCGCG	420		
DB	361	ATCCAGCAGGTCTCGGTGACGCGCACGTGTGCACTCTGACCGGCATGAGTGTGACCGCG	420		
QY	421	TGGTACGTGAGGTGCTTCCTGTCGCGCCCTGACCGCCGACCGCCCGCTGGCGGTG	480		
DB	421	TGGTACGTGAGGTGCTTCCTGTCGCGCCCTGACCGCCGACCGCCCGCTGGCGGTG	480		
QY	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTCGCGCGGTGTCTGCGCCGGTGTCTGCGCCTG	540		
DB	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTCGCGCGGTGTCTGCGCCGGTGTCTGCGCCTG	540		

QY	541	CACCGCCTGTACACCGCGGCGCGCGGCTTCTGAGTGTAGGCTTCCCGACGCGGCGCCTG	600
DB	541	CACCGCCTGTACACCGCGGCGCGCGGCTTCTGAGTGTAGGCTTCCCGACGCGGCGCCTG	600
QY	601	GAGCGCGCTTTCGACACTGTACAACCTGCTGCGCGCTGTACCTGTGCGCGCTCTCGCCACC	660
DB	601	GAGCGCGCTTTCGACACTGTACAACCTGCTGCGCGCTGTACCTGTGCGCGCTCTCGCCACC	660
QY	661	TGCGCCTGTATGCGGCGCATCTGTCGCCACCTGTCGCGCGGTTCGCGTTCGCGCGCGCC	720
DB	661	TGCGCCTGTATGCGGCGCATCTGTCGCCACCTGTCGCGCGGTTCGCGTTCGCGCGCGCC	720
QY	721	GCCGATAGCGCCCTGACAGGGGAGGTCTGTCAGAGCGCGCAGCGCGCTGCGGGCCAAAG	780
DB	721	GCCGATAGCGCCCTGACAGGGGAGGTCTGTCAGAGCGCGCAGCGCGCTGCGGGCCAAAG	780
QY	781	GTCTCGCGGCTGGTGGCGGCGCTGCTGCTCTTCGCGCGCTGCTGGGGGCCCATCCAG	840
DB	781	GTCTCGCGGCTGGTGGCGGCGCTGCTGCTCTTCGCGCGCTGCTGGGGGCCCATCCAG	840
QY	841	CTGTTCTGTGTGTGTCAGGCGCTGGGCGCGCGCGCTCTTGGACACCAACGAGCTACGCC	900
DB	841	CTGTTCTGTGTGTGTCAGGCGCTGGGCGCGCGCGCTCTTGGACACCAACGAGCTACGCC	900
QY	901	GCCTACCGGCTTAAGACCTGGGCTCACTGATGTCCTACAGCAACTCGCGCTGAACCCG	960
DB	901	GCCTACCGGCTTAAGACCTGGGCTCACTGATGTCCTACAGCAACTCGCGCTGAACCCG	960
QY	961	CTGCTCTACGCTTCTTCGGGCTCGCACTTCGACAGAGCTTCGCGCGCGCTGCGCCCTGC	1020
DB	961	CTGCTCTACGCTTCTTCGGGCTCGCACTTCGACAGAGCTTCGCGCGCGCTGCGCCCTGC	1020
QY	1021	GCG	1080
DB	1021	GCG	1080
QY	1081	GCGGAGCTGACACCGCTGGGGTCCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1140
DB	1081	GCGGAGCTGACACCGCTGGGGTCCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1140
QY	1141	AGTGGGCTGGCGCGCGCGCGCGCTGTGCTCTCTGGGGGAGGACAAACGCGCTCTCTGA	1197
DB	1141	AGTGGGCTGGCGCGCGCGCGCGCTGTGCTCTCTGGGGGAGGACAAACGCGCTCTCTGA	1197

RESULT 4

ID	ADN39429	standard; cDNA; 1197 BP.
XX	ADN39429;	
AC	ADN39429;	
XX	17-JUN-2004	(first entry)
XX	Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:A29.	
DE	Human; differential expression; cancer; angiogenic disorder;	
XX	fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;	
KW	inflammatory disease; autoimmune disease;	
KW	retinal neovascularisation syndrome; scarring; uterine fibroid;	
KW	detection; diagnosis; prognosis; drug screening; drug targeting;	
KW	wound healing; contraception; cytostatic; cardiac; immunomodulatory;	
XX	vulnerable; gene therapy; vaccine; gene; ss.	
XX	Homo sapiens.	
XX	WO2003042661-A2.	
PN	22-MAY-2003.	
XX	13-NOV-2002; 2002WO-US036810.	
PF	13-NOV-2001; 2001US-0350666P.	
XX		
XX		
PR		

XX Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
XX WO2003042661-A2.
XX
XX 22-MAY-2003.
XX
XX 13-NOV-2002; 2002WO-US036810.
XX
XX 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0352250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397753P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
XX WPI; 2003-468649/44.
DR P-PSDB; ADN39505.
XX
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosis or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
XX Claim 8; SEQ ID NO A104; 1385pp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosis and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
XX Sequence 1197 BP; 131 A; 481 C; 395 G; 200 T; 0 U; 0 Other;
SQ

Qy 1 ATGCACACCGTGGCTAGTCCGGACCCAAACGCGTCTCTGGGGGGCACCGGCCAACGCTCC 60
Db 1 ATGCACACCGTGGCTAGTCCGGACCCAAACGCGTCTCTGGGGGGCACCGGCCAACGCTCC 60
Qy 61 GGCTGCCCGGGCTGTGGCGCAACGCGCTCGAGACGGCCAGTCCCTTCGCGCGGGCGGTG 120
Db 61 GGCTGCCCGGGCTGTGGCGCAACGCGCTCGAGACGGCCAGTCCCTTCGCGCGGGCGGTG 120
Qy 121 GAGCGCTGGCTGTGGCGCGCTCTTCTTCGCGCGCGTGTATGTCTGTGGGCGCTGGTGGGAAC 180
Db 121 GAGCGCTGGCTGTGGCGCGCTCTTCTTCGCGCGCGTGTATGTCTGTGGGCGCTGGTGGGAAC 180
Qy 181 TCGCTGGTGTATGTACGTCATCTGCGCGCACAAAGCCGATCGGACCGCTTCTTAC 240
Db 181 TCGCTGGTGTATGTACGTCATCTGCGCGCACAAAGCCGATCGGACCGCTTCTTAC 240
Qy 241 ATGCCCAACCTGGCGGCGACGAGCTGACCTTCTCTCTGTGTCTGCTTCCCTTACGGCC 300
Db 241 ATGCCCAACCTGGCGGCGACGAGCTGACCTTCTCTCTGTGTCTGCTTCCCTTACGGCC 300
Qy 301 CTGCTGTACCGCGTGTGCGCGCTGGGTCTGGGCGAGCTTCAATGTGCAAGTTCTGCACTAC 360
Db 301 CTGCTGTACCGCGTGTGCGCGCTGGGTCTGGGCGAGCTTCAATGTGCAAGTTCTGCACTAC 360
Qy 361 ATCCAGCAGGTCTCGGTGAGGCGCACGCTGTGCCACTCTGACCGCATAGTGTGGACCGC 420
Db 361 ATCCAGCAGGTCTCGGTGAGGCGCACGCTGTGCCACTCTGACCGCATAGTGTGGACCGC 420
Qy 421 TGGTACGTGACGGTGTTCCTGCGCGCTGCGCGCGCTGACCGCGCGCGCTTCCCGCGCTG 480
Db 421 TGGTACGTGACGGTGTTCCTGCGCGCTGCGCGCGCTGACCGCGCGCGCTTCCCGCGCTG 480
Qy 481 GCTGTACGCTTACGACATCTGGGTAGGCTCTGCGCGGTGTCTGCGCGGTGTCTGCGCGCTG 540
Db 481 GCTGTACGCTTACGACATCTGGGTAGGCTCTGCGCGGTGTCTGCGCGGTGTCTGCGCGCTG 540
Qy 541 CACCGCTGTACCGCGCGCGCGCTTCTGCGCGCTGACCGCGCGCGCTTCCCGCGCGCGCTG 600
Db 541 CACCGCTGTACCGCGCGCGCGCTTCTGCGCGCTGACCGCGCGCGCTTCCCGCGCGCGCTG 600
Qy 601 GAGCGCGCTTTCGACATGTACAACTCTGCGCGCTGACCTGTCTGCGCGCTGCTGCGCGCTG 660
Db 601 GAGCGCGCTTTCGACATGTACAACTCTGCGCGCTGACCTGTCTGCGCGCTGCTGCGCGCTG 660
Qy 661 TGGCGCTGTATGCGCGCATGTGCGCACCTGCGCGCGGTGTCTGCGCGCGGTGTCTGCGCGCTG 720
Db 661 TGGCGCTGTATGCGCGCATGTGCGCACCTGCGCGCGGTGTCTGCGCGCGGTGTCTGCGCGCTG 720
Qy 721 GCCGATAGCGCGCTTTCGAGGCGCGGTGTCTGCGCGCGGTGTCTGCGCGCGGTGTCTGCGCGCGGTG 780
Db 721 GCCGATAGCGCGCTTTCGAGGCGCGGTGTCTGCGCGCGGTGTCTGCGCGCGGTGTCTGCGCGCGGTG 780
Qy 781 GTCTCGCGCGGTGTGCGCGCGGTGTCTGCTCTTCTGCGCGGTGTCTGCGCGCGGTGTCTGCGCGGTG 840
Db 781 GTCTCGCGCGGTGTGCGCGCGGTGTCTGCTCTTCTGCGCGGTGTCTGCGCGCGGTGTCTGCGCGGTG 840
Qy 841 CTGCTCTGTGTGTCGAGGCGGTGTGCGCGCGGTGTCTGCGCGCGGTGTCTGCGCGCGGTGTCTGCGCGGTG 900
Db 841 CTGCTCTGTGTGTCGAGGCGGTGTGCGCGCGGTGTCTGCGCGCGGTGTCTGCGCGCGGTGTCTGCGCGGTG 900
Qy 901 GCCTACCGCGCTTAAGACCTGGGCTCACTGTATGTCCTACAGCAACTCTGCGCGGTGTGAAACCG 960
Db 901 GCCTACCGCGCTTAAGACCTGGGCTCACTGTATGTCCTACAGCAACTCTGCGCGGTGTGAAACCG 960
Qy 961 CTGCTCTACGCGCTTCTGCGCGGTGTGCGCGGTGTGCGCGCGGTGTGCGCGCGGTGTGCGCGGTG 1020
Db 961 CTGCTCTACGCGCTTCTGCGCGGTGTGCGCGGTGTGCGCGCGGTGTGCGCGCGGTGTGCGCGGTG 1020
Qy 1021 GCG 1080
Db 1021 GCG 1080

Query Match 100.0%; Score 1197; DB 11; Length 1197;
Best Local Similarity 100.0%; Pred. No. 2.2e-167;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 GCGAGCTGCACCGCTGGGTCCACCCCGGCCCCCGCCAGCGGCGCAGAAGCCAGGAGC 1140
 Db |||||
 1081 GCGAGCTGCACCGCTGGGTCCACCCCGGCCCCCGCCAGCGGCGCAGAAGCCAGGAGC 1140
 QY 1141 ACTGGCTGGCGCGCGGCTGTCGCTCTGGGGAGGACAAAGCCCTCTCTGA 1197
 Db |||||
 1141 ACTGGCTGGCGCGCGGCTGTCGCTCTGGGGAGGACAAAGCCCTCTCTGA 1197

RESULT 6
 ADL91584
 ID ADL91584 standard; cDNA; 1197 BP.
 AC ADL91584;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human immune-related polypeptide PRO47351-encoding cDNA, SEQ ID NO:99.
 XX
 KW Human; PRO; activated T cell; immune-related; drug screening; detection;
 KW stimulation; immune response; stimulation; diagnosis; immune-mediated skin disease;
 KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
 KW juvenile chronic arthritis; spondyloarthritis; systemic sclerosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome;
 KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
 KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
 KW immune-mediated renal disease; demyelinating disease;
 KW idiopathic demyelinating polynuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polynuropathy; hepatobiliary disease;
 KW chronic active hepatitis; primary biliary cirrhosis;
 KW granulomatous hepatitis; sclerosing cholangitis;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW Whipple's disease; autoimmune skin disease; immune-mediated skin disease;
 KW bullous skin disease; erythema multiforme; contact dermatitis; psoriasis;
 KW allergic disease; asthma; allergic rhinitis; atopic dermatitis;
 KW food hypersensitivity; urticaria; eosinophilic pneumonia;
 KW idiopathic pulmonary fibrosis; hypersensitivity pneumonitis;
 KW transplantation associated disease; graft rejection;
 KW graft-versus-host disease; immunosuppressive; dermatological;
 KW hepatotropic; nephrotropic; antidiabetic; antiaesthetic; antipsoriatic;
 KW antiallergic; antianemic; antiarteriosclerotic; antiarthritic;
 KW neuroprotective; respiratory; antiinflammatory; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004024072-A2.
 XX
 PD 25-MAR-2004.
 XX
 XX 10-SEP-2003; 2003WO-US028317.
 XX
 PR 11-SEP-2002; 2002US-0410340P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
 PI Williams PM, Wood WI, Wu TD;
 XX
 DR WPI: 2004-329384/30.
 DR P-PSDB; ADU91585.
 XX
 XX New PRO nucleic acid, useful for preparing a composition for diagnosing
 PT or treating an immune related disorder, e.g., systemic lupus
 PT erythematosus in a mammal.
 XX
 PS Claim 2; SEQ ID NO 99; 199pp; English.
 XX
 CC The invention relates to isolated human immune-related polypeptides
 CC (designated PRO) and nucleic acids (ADL91486-ADL91587). The PRO
 CC polypeptides are overexpressed in CD4+ T cells activated by anti-CD3/ICAM
 CC -1 or anti-CD3/anti-CD28 antibodies compared with resting T cells and are
 CC useful as diagnostic markers and therapeutic targets for immune
 CC disorders. The invention also relates to sequences at least 80% identical

CC to the PRO nucleic acid and polypeptide sequences of the invention;
 CC recombinant vectors and host cells comprising a PRO nucleic acid; a
 CC method for the recombinant production of a PRO polypeptide; antibodies
 CC against a PRO polypeptide; fusion proteins comprising a PRO polypeptide;
 CC methods of screening for compounds which modulate PRO polypeptide
 CC activity or expression; a method for detecting a PRO polypeptide; a
 CC method of detecting an immune response in a mammal; and methods for
 CC stimulating an immune response in a mammal; and methods for diagnosing
 CC and treating immune-related disorders. PRO polypeptides and nucleic acids
 CC are useful in the diagnosis and treatment of immune-related disorders
 CC such as systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis, systemic
 CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,
 CC chronic inflammatory demyelinating polynuropathy, hepatobiliary disease,
 CC infectious or autoimmune chronic active hepatitis, primary biliary
 CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory
 CC bowel disease, gluten-sensitive enteropathy, Whipple's disease,
 CC autoimmune or immune-mediated skin disease, bullous skin disease,
 CC erythema multiforme, contact dermatitis, psoriasis, allergic disease,
 CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,
 CC urticaria, immunologic disease of the lung, eosinophilic pneumonias,
 CC idiopathic pulmonary fibrosis, hypersensitivity pneumonitis,
 CC transplantation associated disease, graft rejection or graft-versus-host-
 CC disease. The present sequence represents cDNA encoding a human immune-
 CC related PRO polypeptide of the invention.

XX
 SQ Sequence 1197 BP; 131 A; 481 C; 385 G; 200 T; 0 U; 0 Other;

Query Match
 Best Local Similarity 100.0%; Score 1197; DB 12; Length 1197;
 Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCACACCGGTGGTACGTCCGACCCCAACCGCTCTGGGGGGACCGCCCAACGCTCC 60
 Db |||||
 1 ATGCACACCGGTGGTACGTCCGACCCCAACCGCTCTGGGGGGACCGCCCAACGCTCC 60
 QY 61 GGCTGCCCGGGCTGGGGCCCAACCGCTCGACCGGCCAGTCCCTTCGCCGGGGCCGTG 120
 Db |||||
 61 GGCTGCCCGGGCTGGGGCCCAACCGCTCGACCGGCCAGTCCCTTCGCCGGGGCCGTG 120
 QY 121 GACGCTGGCTCGTGGCGCTCTTCTTGGCGCGCTGTAGTGTCTGGGCTGGTGGGGAAC 180
 Db |||||
 121 GACGCTGGCTCGTGGCGCTCTTCTTGGCGCGCTGTAGTGTCTGGGCTGGTGGGGAAC 180
 QY 181 TCGTGGTCACTACGTCACTGCGCGCCACAAAGCCGATGCGGACCGTGACCAACTTCTAC 240
 Db |||||
 181 TCGTGGTCACTACGTCACTGCGCGCCACAAAGCCGATGCGGACCGTGACCAACTTCTAC 240
 QY 241 ATCGCCAACTGGGGGCCACGAGTGACCTTCTCTGTGTGGTCCCTTTCAGCGCC 300
 Db |||||
 241 ATCGCCAACTGGGGGCCACGAGTGACCTTCTCTGTGTGGTCCCTTTCAGCGCC 300
 QY 301 CTGCTGTACCGCTGCCGGCTGGGTGCTGGCGCACTTCAATGTGCAAGTTTGTCAACTAC 360
 Db |||||
 301 CTGCTGTACCGCTGCCGGCTGGGTGCTGGCGCACTTCAATGTGCAAGTTTGTCAACTAC 360
 QY 361 ATCCAGCAGGCTTCGGTGCAGGCCACGCTGTGCCACTCTGACCGGCATGAGTGTGGACGC 420
 Db |||||
 361 ATCCAGCAGGCTTCGGTGCAGGCCACGCTGTGCCACTCTGACCGGCATGAGTGTGGACGC 420
 QY 421 TGGTACGTGACGGTGTTCCTGGCGCCCTTCACCGCCGACGCCCGCTGGCGCTG 480
 Db |||||
 421 TGGTACGTGACGGTGTTCCTGGCGCCCTTCACCGCCGACGCCCGCTGGCGCTG 480
 QY 481 GCTGTGACGCTCAGCATCTGGGTAGGCTCTCGCGGGTGTCTGGCGCGGTGCTCGCCCTG 540
 Db |||||
 481 GCTGTGACGCTCAGCATCTGGGTAGGCTCTCGCGGGTGTCTGGCGCGGTGCTCGCCCTG 540
 QY 541 CACCGCTGTACCCCGGGCCGCGGCGCTTACTGCGATGAGGGCTTTCGCCAGCGCGCCCTG 600

Db 541 CACCCTGTACCCGGCGCGCCCTACTGCACTGAGGCTTCCCCAGCGCGCCCTG 600
Qy 601 GAGCGCGCTTGGCACTGTACAACTGCTGGCGCTGTACCTGCTGCCCTGCTGCCAC 660
Db 601 GAGCGCGCTTGGCACTGTACAACTGCTGGCGCTGTACCTGCTGCCCTGCTGCCAC 660
Qy 661 TCGCGCTGTATCGCGCATGCTGGCCACCTGTGGCCCGGGTCTGCCCTGCGCCGCGCC 720
Db 661 TCGCGCTGTATCGCGCATGCTGGCCACCTGTGGCCCGGGTCTGCCCTGCGCCGCGCC 720
Qy 721 GCCGATAGCGCTTACAGGGCAGTGTGGCAGAGCGCGAGCGCGCTGGGSCCAAG 780
Db 721 GCCGATAGCGCTTACAGGGCAGTGTGGCAGAGCGCGAGCGCGCTGGGSCCAAG 780
Qy 781 GTCTCGCGCTGTGGCGCGCTGTGTCTCTTTCGCGCGCTGTGTGGGGCCCATCCAG 840
Db 781 GTCTCGCGCTGTGGCGCGCTGTGTCTCTTTCGCGCGCTGTGTGGGGCCCATCCAG 840
Qy 841 CTGTTCTGTGTGCTGACGGCTGTGGCGCGCGCGCGCTCTTGACACCGAGCTACGCC 900
Db 841 CTGTTCTGTGTGCTGACGGCTGTGGCGCGCGCGCGCTCTTGACACCGAGCTACGCC 900
Qy 901 GCTACGCGCTTAAACCTTGGGCTCACTGCACTGTCTTACGCACTCCGCGCTGAACCG 960
Db 901 GCTACGCGCTTAAACCTTGGGCTCACTGCACTGTCTTACGCACTCCGCGCTGAACCG 960
Qy 961 CTGCTTACGCTTCTTGGGCTGCGACTTCGACAGGCTTTCGCGCGCTGTGCCCTGCG 1020
Db 961 CTGCTTACGCTTCTTGGGCTGCGACTTCGACAGGCTTTCGCGCGCTGTGCCCTGCG 1020
Qy 1021 GCG 1080
Db 1021 GCG 1080
Qy 1081 GCGGAGCTGACCGCTTGGGCTTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db 1081 GCGGAGCTGACCGCTTGGGCTTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Qy 1141 AGTGGGCTGGCGCGCGCGCGCTGTGCTCTTGGGGAGGCAACGCGCCCTCTCTGA 1197
Db 1141 AGTGGGCTGGCGCGCGCGCGCTGTGCTCTTGGGGAGGCAACGCGCCCTCTCTGA 1197
RESULT 7
ID ADO29925
AC ADO29925
XX ADO29925;
DT 29-JUL-2004 (first entry)
DE Human GPCR GPR54 polynucleotide, SEQ ID NO:1027.
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antiarthritis;
KW cytosolic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW gene; ss.
OS Homo sapiens.
XX
XX WO2004040000-A2.

XX PD 13-MAY-2004.
XX 09-SEP-2003; 2003WO-US028226.
XX PF 09-SEP-2002; 2002US-0409303P.
XX PR 09-APR-2003; 2003US-0461329P.
XX PA (PRIM-) PRIMAL INC.
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX WPI; 2004-390329/36.
DR P-PSDB; ADO29412.
XX Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.
Claim 151; SEQ ID NO 1027; 542pp; English.
XX The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or vitamin deficiency-related diseases; enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-encoding nucleic acid of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 1197 BP; 131 A; 481 C; 385 G; 200 T; 0 U; 0 Other;
Qy Query Match 100.0%; Score 1197; DB 12; Length 1197;
Best Local Similarity 100.0%; Pred. No. 2.2e-167;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCACACCGTGGCTAGCTCGGACCCCAACGCTTCCTGGGGGGACCGCCCAACGCTCC 60
Db 1 ATGCACACCGTGGCTAGCTCGGACCCCAACGCTTCCTGGGGGGACCGCCCAACGCTCC 60
Qy 61 GGCTGCCCGGCTGTGGCGCCCAACGCTTCGAGCGGCCAGTCCCTTCGCCCGCGGCCGTG 120
Db 61 GGCTGCCCGGCTGTGGCGCCCAACGCTTCGAGCGGCCAGTCCCTTCGCCCGCGGCCGTG 120
Qy 121 GAGCGCTGGCTGTGCGCGCTCTTCTTCGCGCGCTGATGCTGCTGGGCTGTGGGGAAC 180
Db 121 GAGCGCTGGCTGTGCGCGCTCTTCTTCGCGCGCTGATGCTGCTGGGCTGTGGGGAAC 180

[illegible]

RESIN.T 9

ADZ68968

ID ADZ68968 standard; cDNA; 1197 BP.

XX

AC ADZ68968;

XX

DT 14-JUL-2005 (first entry)

XX

uropathic; substrate inhibition; pharmaceutical; genitourinary disease; bladder disease; micturition disorder; prostate hyperplasia; cytostatic; andrology; gynecology and obstetrics; G protein coupled receptor 54; GPR54; KISS1; gene; 58.

Homo sapiens.

Key	Location/Qualifiers
1	1.1
2	2.1
3	3.1
4	4.1
5	5.1
6	6.1
7	7.1
8	8.1
9	9.1
10	10.1
11	11.1
12	12.1
13	13.1
14	14.1
15	15.1
16	16.1
17	17.1
18	18.1
19	19.1
20	20.1
21	21.1
22	22.1
23	23.1
24	24.1
25	25.1
26	26.1
27	27.1
28	28.1
29	29.1
30	30.1
31	31.1
32	32.1
33	33.1
34	34.1
35	35.1
36	36.1
37	37.1
38	38.1
39	39.1
40	40.1
41	41.1
42	42.1
43	43.1
44	44.1
45	45.1
46	46.1
47	47.1
48	48.1
49	49.1
50	50.1
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66	66.1
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72	72.1
73	73.1
74	74.1
75	75.1
76	76.1
77	77.1
78	78.1
79	79.1
80	80.1
81	81.1
82	82.1
83	83.1
84	84.1
85	85.1
86	86.1
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WO2005040833-A1.

06-MAY-2005.

06-OCT-2004: 2004WO-EP011250-

21-OCT-2003: 2003EP-00023850

(ENDD) BAYED HEAT TUNING AG

Verreest C W
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WPI; 2005-355924/
D. DODD. 80250000

Screening for agents that decrease the activity of human metastin recognizing receptors, for treating urological disorders, by contacting a test compound with human metastin recognizing receptor polypeptide or polynucleotide.

Example 1: SEO ID NO 1: 65pp. English

The invention describes a method of screening for agents, which decrease the activity of human metastin recognizing receptor comprising: contacting a test compound with any human metastin recognizing receptor polypeptide or polynucleotide; and detecting binding of the test compound to the human metastin recognizing receptor polypeptide or polynucleotide, where a test compound which binds to the polypeptide or polynucleotide is identified as a potential therapeutic agent and for treating urological disorders. Also described are: a method of screening for agents which regulate the activity of a human metastin recognizing receptor, by contacting a test compound with a human metastin recognizing receptor polypeptide; and detecting a human metastin recognizing receptor activity of the polypeptide, where a test compound which decreases the human metastin recognizing receptor activity of the polypeptide is identified as a potential therapeutic agent for decreasing the activity of the human metastin recognizing receptor and useful to treat urological disorders; a method of reducing the activity of human metastin recognizing receptor, comprising contacting a cell with a reagent which specifically binds to human metastin recognizing receptor polynucleotide or a human metastin recognizing receptor polypeptide, where the activity of human metastin recognizing receptor is reduced and a urological disorder is ameliorated; a reagent that modulates the activity of a human metastin recognizing receptor polypeptide or polynucleotide, where the reagent is identified by the method cited above; and a pharmaceutical composition for the treatment of urological disorders, comprising: the reagent, and a carrier. The methods and compositions are useful for treating urological disorder, such as detrusor overactivity (overactive bladder), urinary incontinence, neurogenic detrusor overactivity (detrusor hyperflexia), idiopathic detrusor overactivity (detrusor instability), benign prostatic hyperplasia, and lower urinary tract symptoms. The reagent is useful in the preparation of a medicament for modulating the activity of human metastin recognizing receptor in a urological disorder. This sequence encodes human G protein coupled receptor 54 (GPR54), a metastin recognising receptor.

Sequence 1197 BP: 131 A: 481 C: 385 G: 200 T: 0 U: 0 Other:

Query Match	Score 1197:	DB 14:	Length 1197:
100.0%	Score 1197:	DB 14:	Length 1197:

2

Best Local Similarity 100.0%; Pred. No. 2.2e-167;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	121	GAGCCCTGGCTCGTGGCGCTCTTCTTCGGCGCGCTGATGCTGCTGGGCTGTGGGGAAC	180
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QY	181	TGCTGGTCACTACGCTACATCGCGCCCAACAGCGATGCGGACCGTGACCAACTTCTAC	240
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QY	661	TGCGCTGTATGCGGCCATGTGCGCCACCTGGGCGGGTGGCGTGGCGCGCGCC	720
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QY	1141	AGTGGGCTGGCGCGCGCGCGCGCTGTGCGCTCTTGGGGGAGCAACGCGCTCTCTGA	1197
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AAA64352			
ID	AAA64352	standard; cDNA; 1197 BP.	
XX			
AC	AAA64352;		
XX			
DT	20-DEC-2000	(first entry)	
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DE		cDNA encoding a human G protein-coupled receptor designated GPR54.	
XX			
KW		Human; GPR54; G protein-coupled receptor; GPCR; eating disorder; obesity;	
KW		Alzheimer's disease; memory; pain; sexual disorder;	
KW		growth hormone imbalance; gene therapy; ss.	
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OS		Homo sapiens.	
XX			
FH		Location/Qualifiers	
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PN		WO200050563-A2.	
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PD		31-AUG-2000.	
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PF		22-FEB-2000; 2000WO-US004416.	
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PR		24-FEB-1999; 99US-0121651P.	
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PA		(MERI) MERCK & CO INC.	
PA		(MERI) MERCK FROSST CANADA & CO.	
PA		(UTOR) UNIV TORONTO.	
XX			
PI		Howard AD, O'Neill GP, O'dowd B, George S;	
XX			
DR		WPI; 2000-572079/53.	
DR		P-PSDB; AAB08540.	
XX			
PT		Novel G protein-coupled receptor resembling galanin receptors useful for	
PT		identifying agonists and antagonists for treating eating disorders;	
PT		obesity, Alzheimer's disease and disorders affecting memory and pain.	
XX			
PS		Claim 2; Fig 1A-B; 52pp; English.	
XX			
CC		The present sequence encodes a human GPR54 protein. The protein is a G	
CC		protein-coupled receptor (GPCR). GPR54 proteins and polynucleotides are	
CC		useful in counter-screens. The DNA molecules can be used in chromosomal	
CC		mapping studies in order to identify the precise chromosomal location of	
CC		the GPR54 gene or of genes encoding proteins related to GPR54. Due to the	
CC		resemblance between GPR54 and the galanin receptors, it is expected that	
CC		agonists and antagonists of GPR54 will be useful for treatment of eating	
CC		disorders and obesity, Alzheimer's disease and other disorders affecting	
CC		memory, pain, sexual disorders and growth hormone imbalances. Gene	
CC		therapy with GPR54 polypeptides is useful for treatment of diseases where	
CC		it is beneficial to elevate GPR54 activity. Nucleotide sequences that are	
CC		complementary to the GPR54 sequences can be synthesized for use in	
CC		antisense therapy. The compounds identified by the assay methods as	
CC		capable of binding to GPR54 act as GPR54 agonists or antagonists that are	
CC		useful as modulators of GPR54 activity	
XX			
SQ		Sequence 1197 BP; 130 A; 481 C; 385 G; 201 T; 0 U; 0 Other;	

Query Match		99.9%;	Score 1195.4;	DB 3;	Length 1197;
Best Local Similarity		99.9%;	Pred. No. 3.7e-167;		
Matches 1196;		Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
Qy	1	ATGCACACCGTGGCTACGTCGGACCCCAACCGCTCTCTGGGGGGACACCGGCCCAACGCCTCC	60		
Db	1	ATGCACACCGTGGCTACGTCGGACCCCAACCGCTCTCTGGGGGGACACCGGCCCAACGCCTCC	60		
Qy	61	GGCTCCCGGGCTGTGGGCGCCAAACCGCTCGAGCGCCCAAGTCCCTTCGCGCGGGCGCGTG	120		
Db	61	GGCTCCCGGGCTGTGGGCGCCAAACCGCTCGAGCGCCCAAGTCCCTTCGCGCGGGCGCGTG	120		
Qy	121	GAGCGCTGCGTGGCGGCTCTCTTCGCGGCGCTGATGCTGGGGCTGTGGGCGCGGAAAC	180		
Db	121	GAGCGCTGGCTGGTGGCGGCTCTCTTCGCGGCGCTGATGCTGGGGCTGTGGGCGCGGAAAC	180		
Qy	181	TGCTGTGGTCACTACGTCATCTGCGCGCCACAGCGGATGCGGACCGTGACCAACTTCTAC	240		
Db	181	TGCTGTGGTCACTACGTCATCTGCGCGCCACAGCGGATGCGGACCGTGACCAACTTCTAC	240		
Qy	241	ATCGCCAACTGGCGGCGCACGAGCATGACCTTCTCTGTGTGCTGCTGCTTCAACGGCC	300		
Db	241	ATCGCCAACTGGCGGCGCACGAGCATGACCTTCTCTGTGTGCTGCTGCTTCAACGGCC	300		
Qy	301	CTGCTGTACCGCTGCGCGGCTGGGTGCTGGGCACTTCATGTGCAAGTTGTCACACTAC	360		
Db	301	CTGCTGTACCGCTGCGCGGCTGGGTGCTGGGCACTTCATGTGCAAGTTGTCACACTAC	360		
Qy	361	ATCCAGCAGGCTCGGTCAGGCCACGCTGTGCACTCTGACCGCCATGAGTGTGACCGC	420		
Db	361	ATCCAGCAGGCTCGGTCAGGCCACGCTGTGCACTCTGACCGCCATGAGTGTGACCGC	420		
Qy	421	TGCTACGTAGCGTGTTCGGTGGCGGCTGTGACCGCGGACGCGCCGCTGGCGGTG	480		
Db	421	TGCTACGTAGCGTGTTCGGTGGCGGCTGTGACCGCGGACGCGCCGCTGGCGGTG	480		
Qy	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTGGGGGGTGTCTGGCGGGTGTCTGGCGGTG	540		
Db	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTGGGGGGTGTCTGGCGGGTGTCTGGCGGTG	540		
Qy	541	CACCGCTGTACCGCGGCGCGGCTTACTGCACTGAGGCTTCTCCCGAGCGCGGCGCTG	600		
Db	541	CACCGCTGTACCGCGGCGCGGCTTACTGCACTGAGGCTTCTCCCGAGCGCGGCGCTG	600		
Qy	601	GAGCGGCTTCGCACTGATACAACTGCTGGGCTGTACCTGCTGCGCGCTGCTGCGCAC	660		
Db	601	GAGCGGCTTCGCACTGATACAACTGCTGGGCTGTACCTGCTGCGCGCTGCTGCGCAC	660		
Qy	661	TGCGCTGCTATGCGGCGCATGCTGCGCACCTGGGCGGGTCTGGCGGCGGCGCGCC	720		
Db	661	TGCGCTGCTATGCGGCGCATGCTGCGCACCTGGGCGGGTCTGGCGGCGGCGCGCC	720		
Qy	721	GCCGATAGCGGCTTCAGGGGAGGTGTGTCAGAGCGCGAGGCGCGCTGGGGCCAAAG	780		
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Qy	781	GTCGCGGCTGTGGGCGCGTGTCTGCTCTTTCGCGGCTGTGGGGCGCCCATCCAG	840		
Db	781	GTCGCGGCTGTGGGCGCGTGTCTGCTCTTTCGCGGCTGTGGGGCGCCCATCCAG	840		
Qy	841	CTGTTCTGTGTGTCAGCGCTGGGCGCCCGGGCTCTCTGGCACCCACGAGCTACGCC	900		
Db	841	CTGTTCTGTGTGTCAGCGCTGGGCGCCCGGGCTCTCTGGCACCCACGAGCTACGCC	900		
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Db	901	GCCTACGGCTTAAGACCTTGGGCTCACTGCACTGTCTTACAGCAACTCCGCGCTGAACCCG	960		
Qy	961	GTGCTCTAGGCTTCTGCGGCTCGACATTCGACAGGCTTTCGCGCGGCTGTGCCCTGTC	1020		
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Qy	1021	GCG	1080		

Db	1021																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
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arthritis, autoimmune diseases, transplant rejection, graft versus host disease, bacterial, fungal, protozoan and viral infections, septicemia, AIDS, pain, psychotic and neurological disorders, including anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, locomotor problems, respiratory disorders, asthma, eating/body weight disorders including obesity, bulimia, diabetes, anorexia, nausea, hypertension, hypotension, vascular and cardiovascular disorders, ischaemia, stroke, cancers, ulcers, urinary retention, sexual/reproductive disorders, circadian rhythm disorders, renal disorders, bone diseases including osteoporosis, benign prostatic hypertrophy, gastrointestinal disorders, nasal congestion, allergies, Parkinson's disease and Alzheimer's disease, and diagnostic assays for such conditions. The present sequence encodes the human SNORF11 receptor

XX Sequence 1197 BP; 130 A; 481 C; 385 G; 201 T; 0 U; 0 Other;

Query Match 99.9%; Score 1195.4; DB 9; Length 1197;
Best Local Similarity 99.9%; Pred. No. 3.7e-167;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 121 GAGCGCTGGCTGTGGGCGCTCTCTTCGCGGGGCTGATGCTGCTGGGCTGTGGGGAAC 180
DB 121 GAGCGCTGGCTGTGGGCGCTCTCTTCGCGGGGCTGATGCTGCTGGGCTGTGGGGAAC 180

QY 181 TCGCTGGTCACTACGTCATCTGCCGCCCAAGCCGATCGGACCGTGACCAACTTCTAC 240
DB 181 TCGCTGGTCACTACGTCATCTGCCGCCCAAGCCGATCGGACCGTGACCAACTTCTAC 240

QY 241 ATGCGCAACCTGGCGGCCAGGAGTGACCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 ATGCGCAACCTGGCGGCCAGGAGTGACCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTG 300

QY 301 CTGCTGTACCGCTGCCCGCTGGGTGCTGGGGGACTTCATGTGCAAGTTCGTCAACTAC 360
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DB 361 ATCCAGCAGCTTCGGTGTGAGGCGACGCTGTGCACCTCTCACCGCATAGTGTGACCGC 420

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DB 421 TGGTACGTGACGCTGTCCGTTGGCGCCCTGCAACCGCCGACGCGCCCTGGCGGTG 480

QY 481 GCTGTGAGCTCAGCATCTGGGTAGGCTCTGGGGGCTGTCTGGCGCGGTGTCTGGCGCTG 540
DB 481 GCTGTGAGCTCAGCATCTGGGTAGGCTCTGGGGGCTGTCTGGCGCGGTGTCTGGCGCTG 540

QY 541 CACCGCTCTGACCGGGCGCGGCTACTGCAAGTGGGCTCTCCCGAGCGCGCCCTG 600
DB 541 CACCGCTCTGACCGGGCGCGGCTACTGCAAGTGGGCTCTCCCGAGCGCGCCCTG 600

QY 601 GAGCGCGCTTCGCACTGTACAACTGTCTGGGCTGTACTCTGCTGCGCTGTCTGCGCAAC 660
DB 601 GAGCGCGCTTCGCACTGTACAACTGTCTGGGCTGTACTCTGCTGCGCTGTCTGCGCAAC 660

QY 661 TGGGCTGTATGCGGCGCATGTCTGGCGCACTGTGGGCGGGTGTGCGTGTGCGCCCGGCC 720
DB 661 TGGGCTGTATGCGGCGCATGTCTGGCGCACTGTGGGCGGGTGTGCGTGTGCGCCCGGCC 720

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QY 781 GTCTCGCGGCTGGTGGCGGCGTGTGCTCTTCTGCGCGCTGTGCTGGGCGCCCATCCAG 840

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DB 1021 GGGCG 1080

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RESULT 14
ADG19756
ID ADG19756 standard; cDNA; 1197 BP.

XX AC ADG19756;
XX DT 26-FEB-2004 (first entry)
XX DE G protein coupled receptor (GPCR) 52872 coding sequence.

XX KW cytosolic; nephrotropic; antiinflammatory; cardiant; respiratory;
KW gastrointestinal; neuroprotective; angiogenesis stimulator; gene therapy;
KW 18636; 2466; 43238; 1983; 52881; 2398; 45449; 50289; 52872; 26908;
KW cellular proliferative disorder; brain disorder; renal disorder;
KW kidney disorder; inflammatory disorder; cardiovascular disorder;
KW liver disorder; intestinal disorder; respiratory disorder;
KW angiogenic disorder; human; G protein coupled receptor; GPCR; gene; ss.

XX OS Homo sapiens.
XX PN US2003215860-A1.
XX PD 20-NOV-2003.
XX PF 03-APR-2003; 2003US-00407079.
XX PR 29-FEB-2000; 2000US-0186059P.
PR 24-MAR-2000; 2000US-0191845P.
PR 22-MAY-2000; 2000US-0206019P.
PR 17-NOV-2000; 2000US-00715790.
PR 28-FEB-2001; 2001US-00796338.
PR 22-MAY-2001; 2001US-00863200.
PR 22-AUG-2001; 2001US-0314041P.
PR 21-AUG-2002; 2002US-00225094.
PR 22-AUG-2002; 2002US-00226102.
PR 15-OCT-2002; 2002US-00272417.
PR 29-OCT-2002; 2002US-00282837.
PR (MILL-) MILLENNIUM PHARM INC.
XX Glucksmann MA, Silos-Santiago I, Carroll JM, Galvin KM;
XX WPI; 2004-010777/01.
XX P-PSDB; ADG19755.
XX DR

[illegible]

DR WPI; 2004-692829/68.
DR P-PSDB; ADS88807.
XX
PT New GPR54 receptor agonists or antagonists, useful for treating
PT gonadotropin related disorders, e.g. hypogonadotropic hypogonadism, or
XX gonadotropin-estradiol/testosterone-dependent related cancers.
PS Disclosure; SEQ ID NO 1; 22pp; English.
XX
CC The specification describes an agonist or antagonist of the GPR54
CC receptor. This agonist or antagonist is used for treating a gonadotropin
CC related disorder. The GPR54 receptor agonist or antagonist is useful for
CC treating a gonadotropin related disorder, such as hypogonadotropic
CC hypogonadism, luteinising hormone (LH) and/or follicle stimulating
CC hormone (FSH) related disorders, or gonadotropin-estradiol/testosterone-
CC dependent related cancers. The present sequence encodes a human GPR54
CC receptor, which is used to identify agonists and antagonists of the
XX invention.
SQ Sequence 1197 BP; 130 A; 481 C; 385 G; 201 T; 0 U; 0 Other;
Query Match 99.9%; Score 1195.4; DB 13; Length 1197;
Best Local Similarity 99.9%; Pred. No. 3.7e-167;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCACACCGTGGCTACGTCCGGACCCCAACCGCTCTCTGGGGGACACCGCCCAACGCTCC 60
Db 1 ATGCACACCGTGGCTACGTCCGGACCCCAACCGCTCTCTGGGGGACACCGCCCAACGCTCC 60
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Job time : 813 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 10_0 , Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	1197	100.0	1197	6	E44032 Novel G pro
3	1197	100.0	1197	6	AR481881 Sequence
4	1197	100.0	1197	6	AX549191 Sequence
5	1197	100.0	1197	8	AB051065 Homo sapi
6	1197	100.0	1197	8	AY029541 Homo sapi
7	1197	100.0	1197	8	AV253981 Homo sapi
8	1197	100.0	1450	6	CQ924743 Sequence
9	1195.4	99.9	1197	6	BD095775 Novel gua
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14	1195.4	99.9	1197	8	HS4309020 Homo sapi
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17	1193.8	99.7	1197	8	AF343725 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS CS081629
DEFINITION Sequence 1 from Patent WO2005040833.
ACCESSION CS081629
VERSION CS081629.1
KEYWORDS GI:66348928
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Yamamoto,N., Matsumoto,H., Hayashi,F. and Tajimi,M.
TITLE Regulation of human metacilin recognising receptors
JOURNAL Patent: WO 2005040833-A 1 06-MAY-2005;
Bayer HealthCare AG (DE)

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AVSLIWVGSAAVSLAHLRSLSPGRAYCSEAPPSRALERAFALYNLLALYLLPL
ATNCYAMLRHLGRVAVRPAPADSLQGVLAERAGNVRKVSRLVANVLLPAACH
GPQLFLVQLAGSWHPSRYAAYALKTWACMSYNSALNPLLVAFLGSHPRQAF
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Sequence 1 from Patent WO2005040833.
CS081629
CS081629.1 GI:66348928

Query Match 100.0%; Score 1197; DB 6; Length 1197;
Best Local Similarity 100.0%; Pred. No. 1.7e-114;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 ATCCAGCAGGTTCGGTGAGGCCACAGTGTGCCACTCTGACCGCATGAGTGTGACCGC 420
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LOCUS AR481881 1197 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 6 from patent US 6699965.
ACCESSION AR481881
VERSION AR481881.1 GI:47243624
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 1197)
AUTHORS Watanabe,T., Terao,Y., Shintani,Y., Ohtaki,T., Kanehashi,K. and Kitada,C.
TITLE Peptides that activate the G-protein coupled receptor protein, JP771175
JOURNAL Patent: US 6699965-A 6 02-MAR-2004;
Takeda Chemical Industries, Ltd.; Osaka;
JPX;
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/organism="unknown"
/mol_type="genomic DNA"
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Query Match 100.0%; Score 1197; DB 6; Length 1197;
Best Local Similarity 100.0%; Pred. No. 1.7e-114; Mismatches 0; Indels 0; Gaps 0;
Matches 1197; Conservative 0;
Qy 1 ATGCACACCGTGGCTACGTCGCGACCCCAACCGCTCGAGCGGCGCACTCGGGGGGACCGCGGCCAACCGCTCC 60
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Db 61 GGCTGCCCGGCTGTGGCGCCAAAGCTTCGAGCGGCGCACTCGCTTCGCGCGGCGCGCGCTG 120
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AX549191 1197 bp DNA linear PAT 26-NOV-2002
LOCUS Sequence 476 from Patent WO02061087.
DEFINITION AX549191
ACCESSION AX549191
VERSION AX549191.1 GI:25813906
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.
1
REFERENCE Burmer,G.C., Roush,C.L. and Brown,J.P.
AUTHORS Antigenic peptides, such as for G protein-coupled receptors
TITLE (GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 476 08-AUG-2002;
FEATURES Lifespan Biosciences, Inc. (US)
source Location/Qualifiers
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Query Match 100.0%; Score 1197; DB 6; Length 1197;
Best Local Similarity 100.0%; Pred. No. 1.7e-114;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5
AB051065 1197 bp mRNA linear PRI 05-JUN-2001
LOCUS Homo sapiens hot7t175 mRNA for G protein-coupled receptor, complete
DEFINITION cda.
ACCESSION AB051065
VERSION AB051065.1 GI:14041797
KEYWORDS

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (sites) Ohtaki,T., Shintani,Y., Honda,S., Matsumoto,H., Hori,A., Kanehashi,K., Terao,Y., Kumano,S., Takatsu,Y., Masuda,Y., Ishibashi,Y., Watanabe,T., Asada,M., Yamada,T., Suenaga,M., Kitada,C., Usuki,S., Kurokawa,T., Onda,H., Nishimura,O. and Fujino,M.
TITLE	Meta2asis suppressor gene KiSS-1 encodes peptide ligand of a G-protein-coupled receptor
JOURNAL	Nature 411 (6837), 613-617 (2001)
PUBMED	11385580
REFERENCE	2 (bases 1 to 1197)
AUTHORS	Shintani,Y., Terao,Y. and Watanabe,T.
TITLE	Direct Submission
JOURNAL	Submitted (12-NOV-2000) Yasushi Shintani, Takeda Chemical Industries, Ltd., Pharmaceutical Discovery Research Division; 10 Wadai, Tsukuba, Ibaraki 300-4293, Japan (E-mail:Shintani.Yasushi@takeda.co.jp, Tel:81-298-64-5011, Fax:81-298-64-5000)
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DEFINITION	Homo sapiens putative G protein-coupled receptor mRNA, complete cds.
ACCESSION	AY029541
VERSION	AY029541.1 GI:15626067
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REFERENCE	1 (bases 1 to 1197)
AUTHORS	Kotani,M., Detheux,M., Vandenbogaerde,A., Communi,D.,

Vanderwinden,J.M., Le Poul,E., Brezillon,S., Tyldesley,R.,
Suarez-Huerta,N., Vandeput,F., Bianpain,C., Schiffmann,S.N.,
Vasart,G. and Parmentier,M.
The metastasis suppressor gene KISS-1 encodes kisseptins, the
natural ligands of the orphan G protein-coupled receptor GPR54
J. Biol. Chem. 276 (37), 34631-34636 (2001)
11457843
2 (bases 1 to 1197)
Kotani,M., Decheux,M. and Parmentier,M.
Direct Submission
Submitted (10-APR-2001) IRIHBN, Universite Libre de Bruxelles, 808,
Route de Lennik, Brussels B-1070, Belgium
Location/Qualifiers

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CDS

ORIGIN

Query Match 100.0%; Score 1197; DB 8; Length 1197;
Best Local Similarity 100.0%; Pred. No. 1.7e-114;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
AY253981 1197 bp mRNA linear PRI 09-MAR-2004
LOCUS
DEFINITION Homo sapiens hypogonadotropin-1 (GPR54) mRNA, complete cds.
ACCESSION AY253981
VERSION AY253981.1 GI:32454259
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1197)
Seminara,S.B., Messager,S., Chatzidakis,E.E., Thresher,R.R.,
Acierno,J.S. Jr., Shagoury,J.K., Bo-Abbas,Y., Kuchung,W.,
Schwinof,K.M., Hendrick,A.G., Zahn,D., Dixon,J., Kaiser,U.B.,
Slaughenaupt,S.A., Guseilla,J.F., O'Rahilly,S., Carlton,M.B.,
Crowley,W.F. Jr., Aparicio,S.A. and Colledge,W.H.
The GPR54 gene as a regulator of puberty
N. Engl. J. Med. 349 (17), 1614-1627 (2003)
14573733
2 (bases 1 to 1197)
Seminara,S.B., Acierno,J.S. Jr., Shagoury,J.K., Bo-Abbas,Y.,
Kuchung,W., Kaiser,U.B., Slaughenaupt,S.A., Guseilla,J.F. and
Crowley,W.F. Jr.
Mutations in a G Protein-coupled Receptor, GPR54, Cause Autosomal
Recessive Idiopathic Hypogonadotropic Hypogonadism

JOURNAL Unpublished (2003)
REFERENCE 3 (bases 1 to 1197)
AUTHORS Seminara,S.B., Acierno,J.S. Jr., Shagoury,J.K., Bo-Abbas,Y.,
Kuohung,W., Kaiser,U.B., Slangenaupt,S.A., Gubella,J.F. and
Crowley,W.F. Jr.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-2003) Reproductive Endocrine Unit, Massachusetts
General Hospital, Bartlett Hall Extension, Room 505, 55 Fruit
Street, Boston, MA 02114, USA
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EDNAPL"

Query Match 100.0%; Score 1197; DB 8; Length 1197;
Best Local Similarity 100.0%; Pred. No. 1.7e-114;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ORIGIN

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DEFINITION Sequence 1 from Patent WO2004098855.
ACCESSION CQ924743
VERSION CQ924743.1 GI:56214300
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
Follettie,M.T.
AUTHORS
METHODS Methods utilising g-protein coupled receptor 54
TITLE Methods utilising g-protein coupled receptor 54
JOURNAL Methods utilising g-protein coupled receptor 54
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ORIGIN

Query Match		100.0%;	Score 1197;	DB 6;	Length 1450;
Best Local Similarity		100.0%;	Pred. No. 1.6e-114;		
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Db	1	ATGCACACCGTGGCTACGTCGCGACCCCAACGCGTCTCTGGGGGGCACCGGCCAACGCTTCC	60		
Qy	61	GGCTGCCCGGCTGTGGCGCCAAAGCTTCGACGCGCCCAAGTCCCTTGGCCCGGGCGGTG	120		
Db	61	GGCTGCCCGGCTGTGGCGCCAAAGCTTCGACGCGCCCAAGTCCCTTGGCCCGGGCGGTG	120		
Qy	121	GACGCTGGCTCGTGGCGCTCTTCTTCGCGGCGCTGATGCTGCTGGGCTGTGGTGGGAAC	180		
Db	121	GACGCTGGCTCGTGGCGCTCTTCTTCGCGGCGCTGATGCTGCTGGGCTGTGGTGGGAAC	180		
Qy	181	TGCTGTGTCATCTACGTCACTGCGGCCACAAAGCGATGCGGACCGTGAACAACTTCTAC	240		
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Qy	241	ATCGCAACCTGGCGGCCACGAGTACCTTCTCTGCTGCTGGTCCCTTTCACGGCC	300		
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Qy	301	CTGCTGTACCGCTGCGCGCTGGTGTGGCGACTTCATGTGCAAGTTCGTCAACTAC	360		
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Qy	361	ATCCAGCAGGTCTCGGTGAGGCCACGCTGTGCCACTCTGACCGCATGAGTGTGGACCGC	420		
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Qy	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGGGGTGTCTGCGCGGTGTCTGCGCCCTG	540		
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Qy	721	GCCGATAGCGCTTCAGGGGAGGTGTGGCAGACGCGAGGCGCGTGTGGGGCCAAAG	780		
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Qy	781	GTCTCGCGCTGGTGGCGCGTGTCTGCTTTCGCGCGCTGTGGGGCCCATTCAG	840		
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Db	1021	GCG	1080		
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LOCUS	BD095775	1197 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use.				
ACCESSION	BD095775				
VERSION	BD095775.1 GI:22641363				
KEYWORDS	WO 0148189-A/33.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1197)				
AUTHORS	Matsumoto, S., Oda, T., Saito, Y., Noriyuki, Morikawa, Yoshida, K., Suwa, M. and Sugiyama, T.				
TITLE	Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use				
JOURNAL	Patent: WO 0148189-A 33 05-JUL-2001; HELIX RESEARCH INSTITUTE, SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO SAITO, NORIYUKI MORIKAWA, KENJI YOSHIDA, MAKIKO SUWA, TOMOYASU SUGIYAMA				
COMMENT	OS Homo sapiens (human) PN WO 0148189-A/33 PD 05-JUL-2001 PF 28-DEC-2000 WO 2000JP009409 PR 28-DEC-1999 JP 99P 375152, 31-MAR-2000 JP 00P 101339 PR 23-MAY-2000 JP 00P 155978 PI SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO SAITO, NORIYUKI PI MORIKAWA, KENJI YOSHIDA, PI MAKIKO SUWA, TOMOYASU SUGIYAMA PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C07K14/705, PC C07K16/28, C12P21/02, C12Q1/02, C12Q1/68, A61K31/711, A61K48/00, A61P43/00, PC G01N33/15, PC G01N33/50 CC Novel guanosine triphosphate-bound protein-coupled receptors CC encoding them, and their production and use CC Key Location/Qualifiers FH 1..1197 FT source /organism='Homo sapiens (human)'. FEATURES source 1..1197 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"				
ORIGIN	Query Match 99.9%; Score 1195.4; DB 6; Length 1197;				

Best Local Similarity 99.9%; Pred. No. 2.5e-114; Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
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RESULT 11
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LOCUS Sequence 1 from Patent EP1464652. linear PAT 17-APR-2005
DEFINITION CQ878955
ACCESSION CQ878955
VERSION CQ878955.1 GI:54033404
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
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AUTHORS De Roux,N., Genin,E., Milgrom,E., Chaussain,J.L. and Carel,J.C.
TITLE GPR54 receptor agonist and antagonist useful for the treatment of gonadotropin related diseases
JOURNAL Patent: EP 1464652-A 1 06-OCT-2004;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); UNIVERSITE PARIS-SUD XI (FR); UNIVERSITE RENE DESCARTES PARIS V (FR)
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ORIGIN
Query Match 99.9%; Score 1195.4; DB 6; Length 1197;
Best Local Similarity 99.9%; Pred. No. 2.5e-114;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DEFINITION Sequence 1 from Patent WO2004087622.
ACCESSION CQ891716
VERSION CQ891716.1 GI:55164312
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS de Roux,N., Genin,E., Milgrom,E., Chaussein,J.L. and Carel,J.C.
TITLE Gpr54 receptor agonist and antagonist useful for the treatment of gonadotropin related diseases
JOURNAL Patent: WO 2004087622-A 1 14-OCT-2004;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); UNIVERSITE RENE DESCARTES (PARIS V) (FR); UNIVERSITE PARIS-SUD (PARIS XI) (FR)
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ORIGIN
Query Match 99.9%; Score 1195.4; DB 6; Length 1197;
Best Local Similarity 99.9%; Pred. No. 2.5e-114;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DEFINITION Sequence 18 from Patent WO0164882.
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VERSION AX239652.1 GI:15797325
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REFERENCE 1 Glucksmann, M.A., Galvin, K.M. and Silos-Santiago, I.
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AUTHORS 1983, 52881, 2396, 45449, 50289, and 52872, G protein-coupled
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TITLE receptors and uses therefor
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JOURNAL Patent: WO 0164882-A 18 07-SEP-2001;
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Millennium Pharmaceuticals, Inc. (US)
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ORIGIN

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Query Match 99.9%; Score 1195.4; DB 6; Length 1197;
Best Local Similarity 99.9%; Pred. No. 2.5e-114;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCACCGTGGCTACGTCGGAGCCCAACGGCTCTGGGGGGACCGCGCAACGCCTCC 60
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AX012 gene; G protein-coupled receptor.
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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Hominidae; Homo.
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Muir, A.I., Chamberlain, L., Elshourbagy, N.A., Michalovich, D.,
Moore, D.J., Calamari, A., Szekeres, P.G., Sarau, H.M., Chambers, J.K.,
Murdoch, P., Steplewski, K., Shabon, U., Miller, J.E., Middleton, S.E.,
```

Darker, J.G., Larminie, C.G., Wilson, S., Bergsma, D.J., Emson, P.,
 Paull, R., Philpott, K.L. and Harrison, D.C.
 AXOR12, a novel human G protein-coupled receptor, activated by the
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 J. Biol. Chem. 276 (31), 28969-28975 (2001)

J. Biol. Chem. 276 (31), 28969-28975 (2001)

11387329

2 (bases 1 to 1197)

Larminie, C.G.C.

Direct Submission

Submitted (29-MAR-2001) Larminie C.G.C., Bioinformatics,
 GlaxoSmithKline, New Frontiers Science Park (North), Third Avenue,
 Harlow, Essex, CM19 5AW, UNITED KINGDOM

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ORIGIN

Query Match 99.9%; Score 1195.4; DB 8; Length 1197;
 Best Local Similarity 99.9%; Pred. No. 2.5e-114;
 Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCACACGTCGTCACGTCGCGACCCACGCGTCCTGGGGGGACCGGCGCCACGCTCC 60
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 1 (bases 1 to 1607)
 Seminars, S.B., Acierno, J.S., Jr., Shagoury, J.K., Bo-Abbas, Y.,
 Kuchung, W., Kaiser, U.B., Slaughter, S.A., Gusek, J.F. and
 Crowley, W.F., Jr.
 Mutations in a G Protein-coupled Receptor, GPR54, Cause Autosomal
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 Unpublished
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 Seminars, S.B., Acierno, J.S., Jr., Shagoury, J.K., Bo-Abbas, Y.,

Kuohung, W., Kaiser, U.B., Slangenhuapt, S.A., Gueella, J.P. and
Crowley, W.F. Jr.
Direct Submission
Submitted (10-MAR-2003) Reproductive Endocrine Unit, Massachusetts
General Hospital, Bartlett Hall Extension, Room 505, 55 Fruit
Street, Boston, MA 02114, USA
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Location/Qualifiers
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ORIGIN

Query Match 99.9%; Score 1195.4; DB 8; Length 1607;
Best Local Similarity 99.9%; Pred. No. 2.2e-114;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 206 GGCTCCCGGGTGTGGGGCCAAACGGCTCGGACCGCCAGTCCCTTCGCCCGGGCCGTG 265
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QY 241 ATGCACAACTGGGGCCACAGGACGTGACCTTCCTCTCTGTGTGGTCCCCTTCACGGCC 300
DB 386 ATGCACAACTGGGGCCACAGGACGTGACCTTCCTCTCTGTGTGGTCCCCTTCACGGCC 445
QY 301 CTGCTGTACCGCTCCCGCTGGGTGTGGGCGACTTTCATGTGCAAGTTCGTCAACTAC 360
DB 446 CTGCTGTACCGCTCCCGCTGGGTGTGGGCGACTTTCATGTGCAAGTTCGTCAACTAC 505
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DB 506 ATCCAGCAGGTCTCGGTGAGGCCACGTGTGCCACTCTGACCGCCATAGTGTGACCGC 565
QY 421 TGGTACGTGACGGTGTTCCTGTGGCGCCCTTGACCGCCGACGCCCGCTGGCGCTG 480
DB 566 TGGTACGTGACGGTGTTCCTGTGGCGCCCTTGACCGCCGACGCCCGCTGGCGCTG 625
QY 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGGCGGGTGTCTGGCGCGGTGTCTGCCCTG 540
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QY 541 CACCGCCTGTACCCCGGGCGCGGCTTACTGTCAGTGAGGCTTCCCCAGCGCGGCGCTG 600

Search completed: February 15, 2006, 04:36:42
Job time : 6323 secs

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QY 661 TGGCCTGTATATGGGCGCATGTGCGCACCTTGGGCGGGTCTGCGCTGCGGCGCGGCCC 720
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DB 866 GCCGATAGCGCCCTTGACAGGGCAGGTCTGCGCAGCGCGCAGCGCGCTGCGGCGCAAG 925
QY 781 GTCTCGCGGCTGTGGCGGCGGCTGTGCTCTTTCGCGCGCTCTGCGGCGCCCATCCAG 840
DB 926 GTCTCGCGGCTGTGGCGGCGGCTGTGCTCTTTCGCGCGCTCTGCGGCGCCCATCCAG 985
QY 841 CTGTTCTGTGTGTCAGGGCGCTGGGCGCCCGCGGCTCTTGGGACCCACGCGAGTACGCC 900
DB 986 CTGTTCTGTGTGTCAGGGCGCTGGGCGCCCGCGGCTCTTGGGACCCACGCGAGTACGCC 1045
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DB 1166 GCG 1225
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QY 1141 AGTGGGCTGGCGCGCGCGCGCTGTGCTCTCTGGGGGAGGACAAACGCGCCCTTCTCTGA 1197
DB 1286 AGTGGGCTGGCGCGCGCGCGCTGTGCTCTCTGGGGGAGGACAAACGCGCCCTTCTCTGA 1342

GenCore version 5.1.1.7
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Run on: February 15, 2006, 03:09:47 ; Search time 332 Seconds
(without alignments)
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Perfect score: 1197
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues
Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
12: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	81.0	67.7	1188	11	US-11-136-527-2760
2	378.8	31.6	600	11	US-11-136-527-6856
3	148.2	12.4	3985	11	US-11-136-527-3404
4	146.2	12.2	1290	11	US-11-136-527-2457
5	146.2	12.2	1290	11	US-11-136-527-6553
6	145.2	12.1	1163	11	US-11-136-527-2458
7	139.4	11.6	1238	7	US-10-995-561-321
8	139.4	11.6	1498	7	US-10-995-561-320
9	139.4	11.6	86131	7	US-10-995-561-13298
10	134.6	11.2	2327	11	US-11-136-527-3190
11	110.2	9.2	1685	7	US-10-750-185-36071
12	110.2	9.2	1885	7	US-10-750-623-36071
13	108.4	9.1	1293	6	US-10-508-892-1
14	108.4	9.1	1293	7	US-10-992-577-7
15	107.4	9.0	1350	11	US-11-136-527-463
16	107.4	9.0	3129	11	US-11-136-527-3314
17	105.8	8.8	1423	11	US-11-136-527-2066
18	99.4	8.3	6244	11	US-11-136-527-3243
19	98.6	8.2	3635	11	US-11-136-527-2101
20	97.8	8.2	79528	7	US-10-276-233A-6
21	94.8	7.9	1584	11	US-11-136-527-2136

22	94	7.9	1410	7	US-10-992-577-1	Sequence 1, Appli
23	90	7.5	1523	11	US-11-137-877-30	Sequence 30, Appl
24	90	7.5	2955	11	US-11-136-527-2954	Sequence 2954, Ap
25	89.4	7.5	2471	11	US-11-136-527-2231	Sequence 2231, Ap
c	86.4	7.2	1224	7	US-10-750-185-40492	Sequence 40492, A
c	86.4	7.2	1224	7	US-10-750-623-40492	Sequence 40492, A
28	85	7.1	1384	11	US-11-136-527-7225	Sequence 2159, Ap
29	83.6	7.0	1400	11	US-11-136-527-7225	Sequence 7225, Ap
30	83.6	7.0	1769	11	US-11-136-527-3129	Sequence 3129, Ap
31	83	6.9	1560	11	US-11-136-527-3742	Sequence 3742, Ap
32	83	6.9	1865	7	US-10-533-355-9	Sequence 9, Appli
33	82.2	6.9	1452	11	US-11-136-527-3122	Sequence 3122, Ap
34	82.2	6.9	2116	11	US-11-136-527-3819	Sequence 3819, Ap
35	79.8	6.7	1524	11	US-11-136-527-3421	Sequence 3421, Ap
36	78.8	6.6	4357	6	US-10-513-118-1	Sequence 1, Appli
37	78.2	6.5	3883	11	US-11-136-527-3673	Sequence 3673, Ap
38	78.2	6.5	4663	11	US-11-136-527-3442	Sequence 3442, Ap
39	77	6.4	1376	7	US-10-502-893-1	Sequence 1, Appli
40	76.8	6.4	1376	7	US-10-627-633-3	Sequence 3, Appli
41	76.2	6.4	600	11	US-11-136-527-6554	Sequence 6554, Ap
42	76.2	6.4	11070	11	US-11-075-185-34	Sequence 34, Appli
43	76.2	6.4	78869	11	US-11-075-185-1	Sequence 1, Appli
44	75.4	6.3	10968	11	US-11-075-185-35	Sequence 35, Appli
45	75.2	6.3	2162	11	US-11-127-877-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1

US-11-136-527-2760
; Sequence 2760, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2760
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2760

Query Match	67.7%	Score 810;	DB 11;	Length 1188;
Best Local Similarity	82.3%	Pred. No. 6.5e-114;		
Matches 953;	Conservative 1;	Mismatches 201;	Indels 3;	Gaps 2;
QY	1	ATGCACACCGTGGCTACGTCGGAGCCCAACCGCTCTCGGGGGCACCGGCCAACGCCTCC	60	
Db	1	ATGCGCGCAGAGGCGACGTTGGTCCGAACGTCGAGCTGGTGGCTCCGTCACACGCTTCG	60	
QY	61	GGCTCCCGGGCTGTTGGGCGCAACCCCTCGAGCGCCAGTCCCTTCGCGGGCGCGCTG	120	
Db	61	GGATCCCGGGCTGCGGTGTCAATGCCCTCGATGGCCAGGCTCGCGCCAGGCCCCCTG	120	
QY	121	GACGCTGGCTGTCGCCCTCTTCTTCGCGGGCTGTGCTGCTGGGCTGTGTGGGGAAC	180	
Db	121	GATGCTGGCTGTCGCCCTCTTCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180	
QY	181	TCGCTGGTCACTACGTCATCTGCGCGCACCAAGCCGATCGCGACCGCTGACCAACTTCTAC	240	
Db	181	TCATGCTGTCATCTGCTTATCTGCGCCACCAAGCACATGACACCGTCCACCAATTTCTAC	240	
QY	241	ATGCGCAACCTGGCGGCGACGAGACGTGCTTCCTTCCTGCTGCTGCTGCTGCTGCTGCTG	300	
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QY 301 CTGCTGTACCGCTGCCCGCTGGGTGCTGGCGACATTCATGTGCAAGTTCTGTCAACTAC 360
Db 301 CTCCTCTATCGCTGCCACCTGGGTGCTGGAGACTTCATGTGCAAAATTCGTCAACTAC 360
QY 361 ATCCAGCAGGTCTCGGTGAGCCACGCTGTGCACCTGTGACCGCATAGTGTGACCGC 420
Db 361 ATCCAGCAGGTCTCGGTGAGCCACATGTGCCACTTTGACAGCATAGTGTGACCGC 420
QY 421 TGGTACGTGACGGTGTCCCGTGTGCGCCCTTGCAACCGCCGACCGCCCGCTGGCGTG 480
Db 421 TGGTACGTGACTGTGTTCCCGCTGCTGCTGCTTACACCGCGCACTTCGCGCGCTGGCCCTG 480
QY 481 GCTGTACGCTCAGCATCTGGTAGGCTCTGGGGCGGTGTCTGGCGCGGTGCTGCGCCCTG 540
Db 481 ACTGTACGCTTAGCATCTGGGTGAGGTTCGCGAGCTGTTCGCGCCCGGTGCTGGCTGTG 540
QY 541 CACGCGCTGTACCGCGCGCGCGCTACTGCACTGAGGCTTCCCGCAGCGCGCGCTG 600
Db 541 CACGCGCTGTGCGCGCGCGCTCACACCTACTGCACTGAGGCTTTCGCGCGCTGGCCCTG 600
QY 601 GAGCGCGCTTTGCGCATCTGACAACCTGTGGCGCTGTACTGCTGCGCGCTGCTGCGCAC 660
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QY 661 TCGCGCTGCTATCGCGCCATGCTGGCGCACTGGCGCGGTGCTGGCGCGCGCGCGCGCC 720
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QY 721 GCGGATAGCGCTTCAGGGGCGAGTGTGGCAGAGCGCGAGCGCGCGTGGGGCCCAAG 780
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QY 901 GCTACGCGCTTAAGACCTGGGCTCACTGCACTGCTTCTGCGCGCTGCTGGGGGCCGACCCG 960
Db 901 GCTACGCGCTCAAGATCTGGGCTCACTGCACTGCTTCTGCGCGCTGCTGGGGGCCGACCCG 957
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Db 961 CTGCTCTATGCTTCTCTGGTTCACACTTCAGACAGGCTTCTGCGCGGTGCTGCGCCCTGC 1017
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Db 1021 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1077
QY 1081 GGGGAGCTGACCGCTGCGGTTCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGC 1140
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QY 1141 AGTGGGCTGGCGCGCGC 1158
Db 1138 CCTGTGGTGCRTCGCC 1155
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RESULT 2

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US-11-136-527-6856
; Sequence 6856, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
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; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6856
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6856
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Query Match

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Best Local Similarity 31.6%; Score 378.8; DB 11; Length 600;
Matches 463; Conservative 1; Mismatches 103; Indels 3; Gaps 2;
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QY 589 AGCGCGCCCTGGAGCGCGCTTCGCACTGTGACAACTGTGTGGCGCTGTACTGTGCGC 648
Db 1 AGCGCGTCCCTGGAGCGCGCTTCGCGCTCTACAACTGTGTGGCGCTGTACTGTGCGC 60
QY 649 CTGCTCGCCACCTGCGCGCTGCTATGCGCCATGTCGCCACCTGGGCGCGGTGCGCGTG 708
Db 61 CTGCTCGCCACCTGCGCGCTGCTACGCTGTCATGCTGGCGCACCTGGGCGCGGTGTA 120
QY 709 CGCGCGCGCGCGCGCGATAGCGCGCTGCAGGGGCGAGTGTGGCAGAGCGCGCAGCGCC 768
Db 121 CGCGCGCGCACCCACTGATGGCGCGCTGCAGGGGCGAGTGTAGCAGAGCGCGCTG 180
QY 769 GTGGGCGCCAAAGTCTCGCGCTGCTGGCGCGCTGCTGGCGCGCTGCTGGCGCGCTG 828
Db 181 GTGGCGCACCAAGTCTCGCGCTGCTGGCGCGCTGCTGGCGCGCTGCTGGCGCGCTG 240
QY 829 GGCGCGCATCCAGCTGCTTCTGGTGTGCTGCGAGCGGTGGCGCGCGCGCGCGCGCT 888
Db 241 GGCGCGCATCCAGCTGCTTCTGGTGTGCTTCAAGCCCT--GCCSCTCGGGGGCTTGG 298
QY 889 CGCAGCTACGCGCGCTACGCGCTTAAGACCTTGGGCTCACTGCACTGTCTACAGCAACTCC 948
Db 299 CGAAGCTATGC-GCTACGCGCTCAAGATCTGGGCTCACTGCACTGTCTACAGCAATTCT 357
QY 949 GCGTGAAACCGCTGCTCTACGCTTCTGCGCTTCTGGGTGCGCATTCGACAGGCTTTCGCGCG 1008
Db 358 GCGTCAACCGCTGCTCTATGCTTCTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 417
QY 1009 GTCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1068
Db 418 GTGTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 477
QY 1069 GCAGCGCCACACGCGGAGCTGCACCGCTGGGGTCCACCGCGCGCGCGCGCGCGCGCG 1128
Db 478 GCGCGACCCCATAGTGTGCGCGCACAGCGGGCTGCGGCACTGCTGCGGGTCAAGACCC 537
QY 1129 AAGCCAGGAGCAGTGGGTGGCGCGCGC 1158
Db 538 GAGCGTGGGAACCTGTGTGCRCTCGCC 567
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RESULT 3

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US-11-136-527-3404
; Sequence 3404, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3404
; LENGTH: 3985
; TYPE: DNA
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; ORGANISM: Rattus norvegicus
US-11-136-527-3404

Query Match      12.4%; Score 148.2; DB 11; Length 3985;
Best Local Similarity 51.5%; Pred. No. 1.6e-14;
Matches 497; Conservative 0; Mismatches 448; Indels 20; Gaps 6;

QY 82 AACGCTCGAGCGGCCAGTCCCTTCGCGCGCGCGCGTGGAGCGCTCGGTCTCGTGGCGCTC 141
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QY 142 TTCTTCGCGCGCTGATGCTGTGCGCTGGTGGGAACTCGTGTGTCATCTACGTGTCATC 201
DB 806 GTGTACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 865
QY 202 TGCAGCCCAAGCCGATGCGGACGCTGACCACTTACATCGCCAACTGCGGCGGCGCAG 261
DB 866 CTGCGGCACAGCTCCAGCCCATCAGTGACAGGTGTCTATATCTCAACCTGGGACTGGCT 925
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DB 926 GAGCAACTCTTCATGCTG---GGCTACCTTCTGCTGCTCAGAACGCCCTGTCTCTAC 982
QY 322 TGGGTGCTGGGCACTTCATGTGCAAGTTGTCACACTACATCAAGCAGGTCTGGTGCAG 381
DB 983 TGGCCCTTTCGGCTCTCTCATGTGTGCTGTGCTGATGGCGGTGGATGGCATCAACAGTTC 1042
QY 382 GCCAGGTGGCACTCTGACCGCCATGAGTGTGGACCGCTGGTGTGAGCGGTGTTCGCG 441
DB 1043 ACCAGCATCTTCGCTCTACCGCTCATGAGTGTGGACCGCTACCTGGCTGTGTGACCCC 1102
QY 442 TTGCGCGCTGTCAGCGCGCGCAGCGCCGCTGGCGCTGGCTGTGAGCTCAGCATCTGCG 501
DB 1103 ACAGCTCTGCGCGCTGGCGCAGCGCACTGTGGCTGCGAATGTTAGTGCAGCTGTCTGG 1162
QY 502 GTAGGCTCTGCGCGGTGTCTGCGCGGTGTCTGCGCTGTGCAACCGCTGTCAACCGGCGG 561
DB 1163 GTGGCTCAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1222
QY 562 CGGCGCTACTGCACTGAG--GCTTCCCAAGCGCGCGCTGTGAGCG--GCTTTCGCACTG 618
DB 1223 AGCAGCTGCCACATGCACTGGCGCAGCGCGCTGTGCGCAACAGCTGTCTATCATC 1282
QY 619 TACAACCTGTGCGCGCTGTACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 678
DB 1283 TATACGCGCGCACTGGGCTTTTGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1342
QY 679 ATGCTGCGCACCTG--GGCGCGGTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 737
DB 1343 ATTGTGTTGAAGTGTGCGGTGACCAACAGCGCGGTGCGCGCGCGCGCGCGCGCGCGGT 1402
QY 738 GGGGAGGTGTGCGCAGAGCGCGCAGCGCGCTGTGCGGCGCAAGGTCTCGCGGCTGGTGGC 797
DB 1403 CAGGCAACCGCTTTCAGCGCGCGCGCGCGCTGTGAGCG--CAGGGTGTACACGATGCTGT 1461
QY 798 GCGCGTGTGCTGCTCTTCTGCGCGCTGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 857
DB 1462 GGTGTGGTGGCACTCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521
QY 858 GCGCTGTGGCGCGCGCGCGCTCTTGGCAGCCAGCGAGCTACGCGCGCTTAAAGAC 917
DB 1522 TGTGGTGTGCGC-----GCTGCGGAGGAGCGCGCTTCTTTGGCGCTTACTT 1569
QY 918 CTGGGCTCATGTGATGCTTACAGCAACTCCGCGCTGAAACCGCGCTGCTTACGCGCTTCT 977
DB 1570 CTGTGTGTGCTGCGCTGCTTACGCCAACAGCTGTGCGCAACCGCGCGCGCGCGCGCGCT 1629
QY 978 GGGCTCGCACTTCGAGCGCTTTCGCGCGCTGCTGCGCGCTGCTGCGCGCGCGCGCGCGCG 1037
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QY 1038 CGGCC 1042

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DB 1690 GAGCC 1694

RESULT 4
US-11-136-527-2457
; Sequence 2457, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2457
; LENGTH: 1290
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2457

Query Match      12.2%; Score 146.2; DB 11; Length 1290;
Best Local Similarity 50.5%; Pred. No. 3.4e-14;
Matches 497; Conservative 0; Mismatches 443; Indels 45; Gaps 4;

QY 52 AACGCTCGGCTGCGCGGTGTGCGCGCAACGCGCTGGACGCGCGCTGATGTGTGCGCG 111
DB 145 AATGCTCGGCGAGCGCGCGCGGAGAACACGAGCCAGGAAGGCGGTAGCGCGCGCTG 204
QY 112 CGGCGCGTGGAGCGCTGCTGCGGCTCTTCTTGGCGCGCTGATGTGTGCGCGCTG 171
DB 205 CAGCGTGGGCGGTC---CTGTACCCCTATTTTTCGCGCTCATCTTCTGCGGCGACC 261
QY 172 GTGGGGAATCGCTGCTCATCTACGCTCATCTGCGCGCAACGCGCATGCGGCGCGTACC 231
DB 262 GTGGGCAACGCTGTGCTGTGCGGTGTGCTGCGCGCGCGCGCGCGCGGTTCAGCACC 321
QY 232 AACTTCTATCGCCAACTGCGCGCACGAGAGTGAACCTTCTCTGTGTGCTGCTGCTG 291
DB 322 AACCTGTTTCTCACTCAACCTGCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 381
QY 292 TTCAAGCGCGCTGCTTACCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 351
DB 382 TTCCAGGCGCAACATCAACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 441
QY 352 GTCAACTATACATCCAGAGCTCTCGGTGCGAGCGCGCTGCTGCTGCTGCTGCTGCTGCT 411
DB 442 GTTCAATTTCTCATCTTTCTCATATGACGCGCAGAGCTTCACGCTGCGCGCGCTCTCC 501
QY 412 GTGGACCGCTGTGACGTGACGCTGTTCCGCTTGGCGCGCTGCTGACCGCGCGCACGCCCG 471
DB 502 CTGGACAGGTATCTGCGCATCCGCTACCGCTGCACTCCGAGAGTTGCGCACACCTCGA 561
QY 472 CTGGCGCTGCTGTGTCAGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTAC 531
DB 562 AACCGCTGCGCGCATCGGCTCATCTGCGGCTAGCAGCTGCTTCTTCTGCGGCGCTTAC 621
QY 532 CTGCGCGCTGCAACCGCTGTCAACCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 591
DB 622 CTGAGCTACTACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
QY 592 CGCGCGCTGAGCGCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651
DB 682 GCACCTCGAGCTGCGAGCATGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
QY 652 CTGCGCACTGCGCGCTGCTTACGCGCGCTGCTGCGCGCTGCTGCGCGCGCTGCTGCGCG 711
DB 742 CTAGTCTCAGTCTGAGCTTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799
QY 712 CCGCGCGCGCGCATAGCGCGCTGCGAGGCGGCTGCTGCGAGAGCGCGCGCGCGCTG 771

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Db 800 -----CGTGACTGAGAGTTCAGGTTCCACGCGGCCAAACG----- 836
Qy 772 CGGGCCAAAGTCTCGCGCTGGTGGCGCGGTGCTGCTTTCGCGCGCTGCTGGGGC 831
Db 837 -----CAAGGTGACAGGATGATCATCTGCGGGTGCCTTTCTGCTCTGTTGGATG 891
Qy 832 CCATCCAGCTGTTCTCTGCTGCTGAGCGCTGGCGCGCGGGGTCTGCGCACCCAGGC 891
Db 892 CCCACCAAGCGCTTATCTCTGCGTGTGGTTCGCT-----TCCCGCTC 939
Qy 892 AGCTACGCGCGCTAGCGCTTAAAGACCTGGGCTCACTGCTACTGCTCCTACAGCAACTCCGCG 951
Db 940 ACGGTGCACTTAGCGCTGGGATCTTTTCACACCTAGTTTCTATGCGCAACTCTCTGT 999
Qy 952 CTGAACCGCTGCTCTACGCTTCTGGGCTGCGACTTTCGACAGGCTTCCGCGCGCTC 1011
Db 1000 GTCAACCCCATCGTTTACGCTCTGCTCTCCAAGCATTTCCGTAAGGTTTCCGCAAAATC 1059
Qy 1012 TGCCCTCGGGCGCGCGCGCGCC 1036
Db 1060 TCGCGGCGCTGCTGCGCGCTGCCCC 1084

RESULT 5

US-11-136-527-6553

; Sequence 6553, Application US/11136527

; Publication No. US20050287570A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6553

; LENGTH: 1290

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-11-136-527-6553

Query Match 12.2%; Score 146.2; DB 11; Length 1290;

Best Local Similarity 50.5%; Pred. No. 3.4e-14;

Matches 497; Conservative 0; Mismatches 443; Indels 45; Gaps 4;

Qy 52 AACGCTCGGCTGCCGGCTGTGGCGCCAAAGCGCTCGGACGGCGCCAGTCCCTTCGCGC 111
Db 145 AATGGCTCCGCGACGCGCGCGGAGAACACGAGCCAGGAGCGGTGAGCGGGCTGG 204
Qy 112 CGGGCGGTGAGCGCTGCTGCTGCGCTCTTCTTCGGGGCGCTGATGCTCTGCGGCTG 171
Db 205 CAGCTGAGGGGTC---CTTGATACCCCTATTTTCGGCGCTCATCTTCTCTGCGGACC 261
Qy 172 GTGGGAACTCGCTGGTGCATCTACGTCTATCGCGCCACAAAGCCGATGCGGACCGTGACC 231
Db 262 GTGGGAAAGCGCTGCTGCGCGTGTGCTGCGCGCGCGCGGCGGTGAGCACCAACC 321
Qy 232 AACTTCTACATCGCAACTGCGCGCCACGAGCGTACCTTCTCTGCTGCTGGTGCCTCC 291
Db 322 AACCTGTTTCATCTCACTCAACCTGGCGGTGGCGACCTGTGTTTCATCTGCTGCTGCT 381
Qy 292 TTCAGGCGCTGCTGTACCGCTGCGCGGTGGGTGCTGGCGAGCTTTCATGTGCAAGTTC 351
Db 382 TTCAGGCGCACTTACACCTGAGACGACTGGGTGTTTCGGCTGCTGCTCTGCAAGCT 441
Qy 352 GTCAACTACATCCAGCAGGTCTCGGTGCGAGGCCAGGTGTCACCTCTGACGCCCATGAT 411
Db 442 GTTCATTCTCTCATCTTTCTCACTATGACGCCAGCAGCTTCACGCTGGCGCGCTCTCC 501

Qy 412 GTGACCGCTGGTACGTGACGGTGTTCCTTCGCGCGCTGACCGCGCGACCGCCGCGC 471
Db 502 CTGACAGAGTATCTGGCCATCCCGCTACCCGCTGACCTCCCGAGAGTTGCGCACACTCGA 561
Qy 472 CTGCGCTGGTGTGTCAGCCTCAGCATCTGGGTAGGCTCTGCGGGGTAGCTGCTCTTC 531
Db 562 AACGCGTGGCGCCATCGGGCTCATCTGGGGGTAGCATGCTCTTCTCCGGGCGCTAC 621
Qy 532 CTGCGCTGACCGCTGTCACCGCGCGCGCGCTCTGACGTAGAGCCTTCCCGAGC 591
Db 622 CTGAGCTACTACCTGACGTGCGCAGTGGCCAACTGACAGTATGCCACCCAGCATGAGC 681
Qy 592 CGCGCTTGGAGCGCGCTTTCGACACTGTAACTGCTGCGCTGACCTGCTGCTGCGCTG 651
Db 682 GCACCTCGAGTGGAGCATGGACCTCTGACCTTCTGTTTACCTACCTGCTGCTGCTG 741
Qy 652 CTGCGCACTGCGCTCTATGCGCCATGCTGCGCCACCTGGCGCGGGTCTGCGCTGCGC 711
Db 742 CTAGTCTCTAGTCTGACCTATGCGGTACCTGCGCTACCTCTGCGCGCACAGTGCACC-- 799
Qy 712 CCGCGCGCGCGGATAGCGCTGTCAGGGGAGGTGCTGGCAGAGCGCGGCGCGCGCTG 771
Db 800 -----CGTGACTGCGAGGTCAGGTTCCACGCGGCCAAACG----- 836
Qy 772 CGGGCCAAAGTCTCGCGCTGGTGGCGCGCTGCTGCTCTTCGCGCGCTGCTGGGGC 831
Db 837 -----CAAGGTGACAGGATGATCATCTGCGGGTGTCTTTCTGCTCTGTTGGATG 891
Qy 832 CCATCCAGCTGTTCTCTGCTGCTGAGCGCTGGCGCGCGGGGTCTGCGCACCCAGGC 891
Db 892 CCCACCAAGCGCTTATCTCTGCGTGTGGTTCGCT-----TCCCGCTC 939
Qy 892 AGCTACGCGCGCTAGCGCTTAAAGACCTGGGCTCACTGCTACTGCTCCTACAGCAACTCCGCG 951
Db 940 ACGGTGCACTTAGCGCTGGGATCTTTTCACACCTAGTTTCTATGCGCAACTCTCTGT 999
Qy 952 CTGAACCGCTGCTCTACGCTTCTGGGCTGCGACTTTCGACAGGCTTCCGCGCGCTC 1011
Db 1000 GTCAACCCCATCGTTTACGCTCTGCTCTCCAAGCATTTCCGTAAGGTTTCCGCAAAATC 1059
Qy 1012 TGCCCTCGGGCGCGCGCGCGCC 1036
Db 1060 TCGCGGCGCTGCTGCGCGCTGCCCC 1084

RESULT 6

US-11-136-527-2458

; Sequence 2458, Application US/11136527

; Publication No. US20050287570A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2458

; LENGTH: 1163

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-11-136-527-2458

Query Match 12.1%; Score 145.2; DB 11; Length 1163;

Best Local Similarity 50.4%; Pred. No. 4.9e-14;

Matches 472; Conservative 5; Mismatches 423; Indels 36; Gaps 4;

Qy 114 GGCGGTGAGCGCTGGGCTGCTGCGCTCTTCTTCGCGCGCTGATGCTGCTGGGCTGGT 173
Db 79 GGCAGTGCCTGTGATCTTTGCCCTCATCTTCTGTTGGCATGTTGGCAATGGCTGGT 138

Qy	174	GGGGAACTCGCTGGTCACTACGTCATCTGCGCGCCACAAGCCGATGCGGACCGTGACCA	233
Db	139	GTTGGCTGTGTACTGCAAGCTTGGCCCAAGTGCCTGGCAGGAGCCAAAGSAGTACCACAGA	198
Qy	234	CTTCTACATCGCAACCTGGGGGCCACGACGTCGACCTTCCCTCCTGTGTGCGTCCCTT	293
Db	199	TCTCTTCACTCACTTGGCCGTGGCCGACCTTTGCTTTCATCTGTGTGCGTGCCTT	258
Qy	294	CACGGCCCTGTGTACCCGCTGCCCGCTGGGTGTGGCGCATCTCATGTGCAAGTTCGT	353
Db	259	CCAGCAGCCTCTACACACTGGATGCTGCTCTTTGGGGCTTTTCGTGTGCAAGACGT	318
Qy	354	CAACTACATCCAGCAGGTCTCGGTGACGCGCACGTCCTGCACTGTGACCGCCATGATGT	413
Db	319	ACATCTGCTCATCTACCTTCAACATGATGCCAGCAGCTTCACTTGTGGCGCGCTCCCT	378
Qy	414	GGACCGCTGGTACGTGACGGGTGTTCCCGTTGGCGGCCCTTGACCCGCGCCACGCCCCGCT	473
Db	379	GGACAGGTACCTGGCTGTGGCGCACCMACCTGCCTCCAGAGCCCTCGCACCCCGGCNA	438
Qy	474	GGCGTGTGCTGTACGCTCAGCATCTGGGTGAGGCTCTGGGGCGGTGTCTGCGCCGGTGT	533
Db	439	CGCGCGCCGCGCTGGGGCTCGTGTGGCTGTGGCGGCTCTCTTTTCGCGCCCTACCT	498
Qy	534	CGCCCTGCACCGCCTGTCAACCGGGCCGCGGCCCTACTGCAGTGAAGGCTTCCCCAGCG	593
Db	499	AAGCTATYACGGCACGGTGCCTACGGCGCGCTCGAGCTCTGCGTGCCTTGGGAGGA	558
Qy	594	CGCCCTGGAGCGCGCTTTCGCACCTGTACAACCTGTGCGCTGTACTGTCTGCCCTGTCT	653
Db	559	CGCGGGCGCGCGCTGTGACGTGGCCACCTTTCGCGGGCTACTGTCTGCCGTGGC	618
Qy	654	CGCCACCTGCGCTGTATGCGGCCCATGTGCGCCACTGTGGCGGGTGCCTGCGGCC	713
Db	619	CGTGTGAGCCTGGCTACGGACGACGCTATGTTTCTCT---ATGGCGCGCGTGGGTCC	675
Qy	714	CGCGCCCGCCATAGCGCCCTGCAGGGCAGGTGTGGCAGAGCGCGCAGGCGCGTGGC	773
Db	676	CGC-----GGGCGCGCGCGCAGAGGCGCGCAGACGGGCGACCGCGCGGGCG	724
Qy	774	GGCCAAAGTCTCGCGCTGTGGCGCGCTGTCTCTGTCTTCGCGCGCTGTCTGGGGCC	833
Db	725	GG-----ACSGGCCATGCTGGCAGTGGCGCGCTCTACGCGCTTGTCTGGGGCC	774
Qy	834	CATCCAGTGTTCCTGTGTGTGACGGCGCTGGGCCCCCGGGCTCCTGECACCCACGAG	893
Db	775	GCACACCGCTCAT-----CCTCTGCTTCTGTGTACGGYCGCTTGCCTTCAG	822
Qy	894	CTAGCGCGCCTACGGCTTAAGACCTGGGGCTCACTGCATGTCTTACAGCACTCCGCGT	953
Db	823	CCCGGCCACCTACGCTCTGCGCTGGCTTCGCACTGCTCGCTCTACGCACTCTGCTGT	882
Qy	954	GAACCCGCTGTCTACGCTTCTCTGGGTTCGCACTTTCGACAGAGGCTTTCGCGCGGTCTG	1011
Db	883	TAAACCGCTCTGTACTCGCTCGCCTCGCGCACCTTCGCGCGCGCTTTCGCGCGCTGTG	942
Qy	1014	CCCTGCGCGCGCGCGCCCGCCCGCCCGCGCCCGCGCGCG	1049
Db	943	GCCCTGCGCGGTGTGCGGCCACCGCCACGACACCG	978

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: CURRENT FILING DATE: 2004-11-24
: NUMBER OF SEQ ID NOS: 85702
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 321
: LENGTH: 1238
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-995-561-321

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Query Match	11.6%	Score 139.4	DB 7	Length 1238
Best Local Similarity	52.1%	Pred. No. 3.6e-13		
Matches 377	Conservative 5	Mismatches 326	Indels 15	Gaps 3
Qy	2	TGCACACGCTGGCTACGTCGCGACCCACACGGCTCCTGGGGGACCGGACCGGCAACGCTCCG	61	
Db	91	TGCCCCCGGGGCGAGAGGGCTGGGACGGCTGGCCCTCTCGAGCCATGCCAGTA	150	
Qy	62	GCTGCCCGGGCTGTGGGCCCAACGCCTCGGACGGCCCAAGTCCTTCCTGGCGCGGGCGGTGG	121	
Db	151	GCGCTCCGCGGGAGCGGAGGAGCGGTGGCGGGGCC---CGGGACGCGCGCGGGCGCGG	207	
Qy	122	ACGCCTGGCTCGTGCCTCTTCTTCGGGGGCTGATGCTGTGGGCTGTGTGGGGAACCT	181	
Db	208	GCATGTGCTGATACAGTGCACTACGCGCTGTGTGCTGTGGGGCTGTGTGGGCAACG	267	
Qy	182	CGTGTGTCACTACGTCACTTGC CGCCACAAAGCCGATGCGACCGCTGACCAACTTCTACA	241	
Db	268	CCCTGGTCACTTCGTGATCTTCGTACGCCAAGATGAAGCGCTACCAACATCTACC	327	
Qy	242	TGCGCAACCTGGCGGCCACGGAAGTGACCTTTCCTCTCTGTGTGTGCTGCCCTTTCACGGGCC	301	
Db	328	TGCTCAACCTGGCGGTACGCCACGAGCTTTCATGCTG---AGCGTGCCCTTCGTGGCCT	384	
Qy	302	TGCTGTACCGCTGSCCGCGCTGGGTGTGGGGCACTTCATGTGCAAGTTCTGTCAACTACA	361	
Db	385	CGTCGGCGCCCTCGCCACCTTGGCCCTTCGGCTCCGTCTGTGCCGCGGTGCTCAGCG	444	
Qy	362	TCCAGCAGGTCTCGGTGCAGGCCACGTGTGCACTCTGACCGCCATGAGTGTGGACCGCT	421	
Db	445	TCGACGGCCTCAACATGTTACACAGCGTTCCTGTCTCACCGTGTGACGGTGGACCGCT	504	
Qy	422	GGTACGTGAAGGTGTTCCGTTTGGCGGCCCTGTGACCCGCGCACGCCCGCTTGGCGCTGG	481	
Db	505	ACGTGGCGGTGTGACGCTCTGGCGCGGGGACCTACCGCGGGCCGACGCTGGGCCAAGC	564	
Qy	482	CTGTGACGCTCAGCATCTGGGTAGCTCTGCGGGGTGTGTGCGCCGCTGTCTGCGCCTCG	541	
Db	565	TCATCAACCTGGGGGTGTGGCTTGGCATCCCTGTGTGTCACTCTCCCATTCGCATCTTCG	624	
Qy	542	ACCGCTGTACCCGGGCGCGCCCTA-----CTGCAGTAGGCGCTTCCCGACGC	592	
Db	625	CAGACACAGACCGGCTCGCGGGCCACGGCGCTGGCCCTTGCAACCTGCAGTGGCCACACC	684	
Qy	593	GCGCCCTGGAGCGGCTTTCGCACTGTACAACTGTCTGGCGCTGTACCTGTCTGGCGCTGC	652	
Db	685	GCGCCTGTGCGCAATTTTCGTGTGTACACTTTTCTCTGCTGGGCTTCTGTCTGCGCGTGC	744	
Qy	653	TGCGCACTCGGCTGTATGCGGCCCATGCTGTGCGCACTGTGGCGCGGCTGCGCGCTGCGCC	712	
Db	745	TGGCCATTGGTGTGTACTCTGTCTCATCTGTGGGCAAGATGCGCGCGCTGCGCCCTGCGG	804	
Qy	713	CCG	715	
Db	805	MKG	807	

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RESULT 8
US-10-995-561-320
; Sequence 320, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

```

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 320
; LENGTH: 1498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-320

Query Match 11.6%; Score 139.4; DB 7; Length 1498;
Best Local Similarity 52.1%; Pred. No. 3.6e-13;
Matches 377; Conservative 5; Mismatches 326; Indels 15; Gaps 3;
QY 2 TGCACACGCTGCTACGTCGCGACCCACGCGTCTCGGGGGACCGGCCAACGCTCCG 61
Db 91 TGCACACGCTGCTACGTCGCGACCCACGCGTCTCGGGGGACCGGCCAACGCTCCG 150
QY 62 GCTGCTCCGGGCTGTGGCGCCAAACGCTCTCGGACGGCCCAAGTCCCTTCGCGCGGGCGGTGG 121
Db 151 GCGCTCCGGGAGCGAGAGGCGGTGGCGGGCC---CGGGACGCGCGGGCGG 207
QY 122 AGCGCTGGCTCGTGGCGCTCTTCTTCGCGGGCGGTGATGCTGCTGGCGCTGTGGGGAAC 181
Db 208 GCATGGTGCCTATCCAGTGCATCTACGCGCTGGTGTGCTGTGGGGGTGGTGGGCAACG 267
QY 182 CGCTGGTGCATCTACGTGCATCTGCGCCCAAGCGATGCGGACCGTACCAACCTTCTACA 241
Db 268 CCCTGGTGCATCTTCTGTATCTTCTGCTACGCAAGATGAAAGCGCTACCAACATCTACC 327
QY 242 TCGCAACCTGGCGGCCACGACGTGACCTTCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTG 301
Db 328 TGCTCAACCTGGCGGTAGCGGACGAGCTTTCATGCTG---AGCGTGGCTTCGTGGCT 384
QY 302 TGCTGTACCGCTGCGCGGCTGGGTGCTGGGGGACCTTATGTCGAGTTCGTCACATACA 361
Db 385 GCTGGCGCGCTGCGCCACTGGCCCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
QY 362 TCCAGCAGGTCTCGGTGACGCGCAGGTGTCACCTCTGACCGCATGAGTGTGACACGCT 421
Db 445 TCGACGGCTCAACATGTTACAGCGCTTCTGTCTCACCCTGCTCAGCTGACGCTGACCGCT 504
QY 422 GGTACGTGACGGTGTCCGTTGGCGCCCTGCAACCGCGCACCGCCCGCTGGCGCTGG 481
Db 505 ACGTGGCGGTGTGACACCTCTGCGCGCGCGACCTACCGCGCGCCAGCGTGGCCAAAGC 564
QY 482 CTGTACGCTCAGCATCTGGGTAGGCTCTGCGGGGTGTCTGCGCGGTGCTGCGCCCTGC 541
Db 565 TCATCAACCTGGCGGTGTGGTGGCATCCCTGTTGGTCACTCTCCCATGCCATCTTCG 624
QY 542 ACCGCTGTACCGGGCGCGCGCTA-----CTGCAGTGAGGCTTCCCGAGCC 592
Db 625 CAGACACAGACCGGCTCGCGCGGCGCAGGCGGTGGCTGCAACTGTCAGTGGCCACACC 684
QY 593 CGCGCTTGGAGCGCGCTTCGACCTGTATCAACCTGCTGGCGCTGTACCTGTGCGGCTGC 652
Db 685 CGGCTGTGCGCAGTCTTGGTGTCTACATTTCTCTGCTGGCTTCTGCTGCGCGCTGC 744
QY 653 TCGCCACCTGGCGCTGTATGGGCGCATGCTGGCGCATGCTGGCGCGGTGCTGCGCGCTGC 712
Db 745 TGGCCATGGTGTGTGCTACCTGTCTCATCTGTTGGCAAGATGCGCGCGCTGCGCGCTG 804
QY 713 CCG 715
Db 805 MKG 807

RESULT 9
US-10-995-561-13298
; Sequence 13298, Application US/10995561

; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13298
; LENGTH: 86131
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13298

Query Match 11.6%; Score 139.4; DB 7; Length 86131;
Best Local Similarity 52.1%; Pred. No. 2.8e-13;
Matches 377; Conservative 5; Mismatches 326; Indels 15; Gaps 3;
QY 2 TGCACACGCTGCTACGTCGCGACCCACGCGTCTCGGGGGACCGGCCAACGCTCCG 61
Db 6092 TGCACACGCTGCTACGTCGCGACCCACGCGTCTCGGGGGACCGGCCAACGCTCCG 6151
QY 62 GCTGCTCCGGGCTGTGGCGCCAAACGCTCTGAGACGCCAGTCCCTTCGCGCGGGCGGTGG 121
Db 6152 GCGCTCCGGGAGCGAGGAGCGGTGGCGGGCC---CGGGACGCGCGGGCGGCGG 6208
QY 122 AGCGCTGGCTCGTGGCGCTCTTCTTCGCGGGCTGATGCTGCTGGGCTGTGGGGAAC 181
Db 6209 GCATGGTGCCTATCCAGTGCATCTACGCGCTGTGCTGCTGGTGGGCTGTGGGCAACG 6268
QY 182 CGCTGGTGCATCTACGTGCATCTGCGCCCAAGCGATGCGGACCGTACCAACCTTCTACA 241
Db 6269 CCCTGGTGCATCTTCTGTATCTTCTGCTAGCACAAGATGAAGACGGCTACCAACATCTACC 6328
QY 242 TCGCAACCTGGCGGCCACGACGTGACCTTCTCTGCTGTGCTGCTGCTGCTGCTGCTG 301
Db 6329 TGCTCAACCTGGCGGTAGCGGACGAGCTTTCATGCTG---AGCGTGGCTTCTGGGCT 6385
QY 302 TGCTGTACCGCTGCTCCCGGCTGGGTGCTGGCGGACTTTCATGCAAGTTCGTCAACTACA 361
Db 6386 CGTGGCGCGCTCGGCCACTGGGCCCTTCGGCTCGGTGCTGTGCGCGCGGTGCTCAGCG 6445
QY 362 TCCAGCAGGTCTCGGTGACGCGCACGTTGTCACCTCTGACCGCATGAGTGTGACACGCT 421
Db 6446 TCGACGGCTCAACATGTTTACACAGCGCTTCTGCTCACCCTGCTCAGCGTGGACCGCT 6505
QY 422 GGTACGTGACGGTGTTCGTTGGCGGCCCTGCAACCGCGCACCGCCCGCTTGGGCTGG 481
Db 6506 ACGTGGCGGTGTGACACCTCTGCGCGGGGACCTACCGCGCGCCAGCGTGGCCAAAGC 6565
QY 482 CTGTACGCTCAGCATCTGGGTAGGCTCTGCGGGGTGTCTGCGCGGTGCTGCGCCCTGC 541
Db 6566 TCATCAACCTGGCGGTGTGGCTGGCATCCCTGTTGGTCACTCTCCCATGCCATCTTTCG 6625
QY 542 ACCGCTGTACCGGGCGCGCGCTA-----CTGCAGTGAGGCTTCCCGAGCC 592
Db 6626 CAGACACAGACCGGCTCGCGCGGCGCAGGCGGTGGCTGCAACTGTCAGTGGCCACACC 6685
QY 593 CGCGCTTGGAGCGCGCTTTCGACCTGTATCAACCTGCTGGCGCTGTACTGCTGCGGCTGC 652
Db 6686 CGGCTGTGCGCAGTCTTGGTGTCTACATTTCTCTGCTGGGTTCCTGCTGCGCGCTGC 6745
QY 653 TCGCCACCTGGCGCTGTATGCGGCCATGCTGCGCCACTGTCGGCGGGGTGCTGCGGTGCGCC 712
Db 6746 TGGCCATGGTGTGTGCTACCTGTCTCATCTGTTGGCAAGATGCGCGCGGTGCGCGCTG 6805
QY 713 CCG 715
Db 6806 MKG 6808

RESULT 10	
US-11-136-527-3190	
; Sequence 3190, Application US/11136527	
; Publication No. US20050287570A1	
; GENERAL INFORMATION:	
; APPLICANT: Wyeth	
; APPLICANT: Mounts, William M	
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes	
; FILE REFERENCE: 031896-041000 (AM101086)	
; CURRENT APPLICATION NUMBER: US/11/136,527	
; CURRENT FILING DATE: 2005-05-25	
; PRIOR APPLICATION NUMBER: US 60/574,294	
; PRIOR FILING DATE: 2005-05-26	
; NUMBER OF SEQ ID NOS: 362830	
; SOFTWARE: PatentIn version 3.2	
; SEQ ID NO 3190	
; LENGTH: 2327	
; TYPE: DNA	
; ORGANISM: Rattus norvegicus	
US-11-136-527-3190	
Query Match	11.2%; Score 134.6; DB 11; Length 2327;
Best Local Similarity	55.3%; Pred. No. 1.8e-12;
Matches 328; Conservative 1; Mismatches 250; Indels 14; Gaps 3	
QY	115 GCCGTGGACGCGCTGGCTCGTCCGCGCTCTTTTCGCGCGCGCTGATGCTGCTGGCGCTGGT 174
Db	327 GCGGTGGAGAACTTCATCACGCTGGTGGTGTTCGCGCTTAATTTCCGCGATGGCGGTGCTG 386
QY	175 GGGAACTCGCTGGTGCATCTAGCTCATCTGCGGCCCAAGCC-----GATCGGGACCGCTG 228
Db	387 GGCAACAGCCTGGTGATCACCGTGTGCGCGCAGCAAAACCGGCAAGCCGCGCAGCACC 446
QY	229 ACCAACTTCTAATCGCCAACTTGGCGGCGCAGGACGTGACCTTCCTCTGCTGCTGCGTC 288
Db	447 ACCAACTCTGTTTCATCCTCAACTCGAGCATCGCAGACCTGGSGCTACTCTCTCTTCGTGCATC 506
QY	289 CCCTTACGGCCCTGCTGTATCCCGCTGCCGCTGGGTGGTGGGGGACCTTCATGTGCAAG 348
Db	507 CCTTTCAGGCCACCGTGTACGACTGCCCACTGGGTGCTGGGGGCGCTTCATCTGCAGG 566
QY	349 TTCGTCAACTATCATCAGCAGGTCTCGGTGACAGGCCACGTGTGCCACTCTGACCGCCCATG 408
Db	567 TTTATACACTACTTCTTACCGTGTCCATGTCTGTGACATCTTCACCTTGGCCGCGATG 626
QY	409 AGTGTGACCGCTGCTACGTGACGGTGTTCGCGTTCGCGGCCCTGTGCACCGCGCAGCACC 468
Db	627 TCTGTGGATCGCTATGTGGCCATTGTGCAATTCACGGCGCTCTCTCCTCCTCAGGGTGTCC 686
QY	469 GGCCTGGCGGTGGCT--GTACGCTCTCAGCATCTGGGTAGGCTCTCGGGCGGTGTCTGGCC 526
Db	687 CGCCAAACGCGCTGTGCGGCGTGGGCGCTTCATCTGGGCGCTGTCCATCGCTATGGCCTCGC 746
QY	527 CGGTGCTCGCCCTGCACCGCTGTCCACCGGCGCGCGC-----GCCTACTGCACTGAGG 580
Db	747 CGGTGGCTACTACGAGCGCCTTTTTCATCGGGACAGCAACCAACCTTCTGCTGGGAGC 806
QY	581 CTTTCCCCAGCGCGCCCTGGAGCGCGCTTCCTGCACACTGTACAACCTGCTGGCGCTGTACC 640
Db	807 ACTGGCCCCAACCACTCCACGAAGGCTTACGTGGTGTGCACATTTTCGTTCTTTGTTTACC 866
QY	641 TGCTGCGGCTGCTGCGCACCTGCGGCTGCTATGCGGCCCATGCTGGGCCACCTG 693
Db	867 TTCTGCCCTTACTGCTCATCTGCTTTTTCGCTATGCGCAAGGTTCTCAATCATCTG 919

RESULT 11
US-10-750-185-36071/c
; Sequence 36071, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.

```

; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 36071
; LENGTH: 1685
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-36071

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Query Match	9.2%; Score 110.2; DB 7; Length 1685;
Best Local Similarity	51.6%; Pred. No. 8.7e-09;
Matches	312; Conservative 0; Mismatches 278; Indels 15; Gaps 2;
Qy	123 CGCTGGCTCGTGCCGCTCTCTTCGGGGCGCTGATGCTGCTGGGCTGTGGGAACTC 182
Db	
1342	CGTATACCTCATCTCTTTTCACTACTCCGTGGTGTGCTCGGTGGGGCTCTGTGGGAACTC 1283
Qy	183 GCTGGTCATCTAGCTCATCTCGCGCCAAAGCCGATGCGGACCGTGCAGCAACTTCTACAT 242
Db	
1282	CATGGTCATCTAGTATCTGTGCTACGCCAAGATGAAGCGGCCAACATCTACAT 1223
Qy	243 CGCCAACTCGCGGCCACGGACGTACCTTCTCTGTGTGCTGCCCTCCCTTCACGGCCCT 302
Db	
1222	CCTCAACTGGCCATCGCCGATGAG--CTGCTCATGCTCAGCGTGCCCTTCTGTGGTCA 1166
Qy	303 GCTGTACCCTGCTGCCGGCTGGGTGCTGGGCGACTTCATGTGCAGTTTCGTCAACTACAT 362
Db	
1165	CTCCACATTTGTTTCGCCACTGGCCCTTCGGCGGGCTACTCTGCCGCTCGTGTCTCAGCGT 1106
Qy	363 CCAGCAGGCTCTCGGTGCAGGCCACGTTGTCACCTCTGCACGCCATGATGTGCACCGCTG 422
Db	
1105	GGAGCAGTCAACATGTTTCAACAGACTCTACTGTCTGACTGTGCTTAGCGTGCACCGCTA 1046
Qy	423 GTACGTGACGGTGTTCOCGTTGGCGGCCCTGCACCGCGCACGCCCGCTGGCGCTGGCG 482
Db	
1045	CGTGGCGTGGTGCACCCCATCAAGCCGCA CGCTACCGCGGCCACCGTGCCCAAGGT 986
Qy	483 TGTGAGCCTCAGCATCTGGGTAGGCTGTGCGGGGTGTCTGCGCCGGTGTCTGCCCTGCA 542
Db	
985	GGTGAATCTGGGCGTGTGGGTGTGTGCTGCTCGTCTCATCTGCCCATCTGGGTCTTCTC 926
Qy	543 CCGCTGTCACC-----CGGGCCGCGGGCTACTGCAGTGAGGCTTCCCCAG 590
Db	
925	GCGCAGCGGGCCAAACAGACGCGCACGTTGGCTGCAACTGCTCATGCCAGGCCCGC 866
Qy	591 CCGCGCCCTGAGCGGCCCTTTCACCTGTACAACTGCTGGCGGTGTACTGCTGTCCGCT 650
Db	
865	CCAGCGCTGGCTGTGGGCTTCGTGTTGTACATTTCTCATGGGCTTCTGCTGCCCGT 806
Qy	651 GCTCGCCACTTGGCCCTGTCTATCGGCCCATGTCTGCGCACCTGGGGCGGGTCCGCGTGG 710
Db	
805	CGGGCCATCTGCTGTGTCTACGTGTCTCATCGCCAAATGGCATGTGGCCCTCAA 746
Qy	711 CCCC 715
Db	
745	GGCC 741

RESULT 12
US-10-750-623-36071/c
; Sequence 36071, Application US/10750623
; Publication No. US20050287531A1

```
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36071
; LENGTH: 1685
; TYPE: DNA
; ORGANISM: Bovine 19866880675545
US-10-750-623-36071

Query Match      9.2%; Score 110.2; DB 7; Length 1685;
Best Local Similarity 51.6%; Pred. No. 8.7e-09;
Matches 312; Conservative 0; Mismatches 278; Indels 15; Gaps 2;

Qy 123 CGCTTGGCTGTGGCGCTCTTCTTGGCGGCGCTGATGCTGTGGCCCTGGTGGGGAATC 182
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1342 CGCTATCTCATCTCTTTTCATCTACTCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1283
Qy 183 GCTGGTATCTACGTCACTCGCCCAACAGCCGATGGGACCGTGACCACTTCTACAT 242
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1282 CATGGTCACTACGTGATCTCGCGCTACGCCAAGATGAAGACGGCCACCAATCTACAT 1223
Qy 243 CGCCAACTGGCGGCGACGAGCTTCTCTCTGTGCTGCGCTTTCACGGCCCT 302
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1222 CTTCACTTGGCTATCGCCGATGAG---CTGCTATGCTAGCGTGCCCTTCTTGGTCA 1166
Qy 303 GCTGTACCCGCTGCGCGCTGGTGTGGGCGACTTCAATGCAAGTTGCTCAATACAT 362
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1165 CTCACATGCTTGCACACTGGCCCTTGGCGCGCTACTCTGCGCCCTCGTGTCAAGGT 1106
Qy 363 CCAGCAGTCTCGGTGACAGGCGACGTGTGCACCTGTACCCGCGATGAGTGTGGACCG 422
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1105 GGACGCACTCAACATGTTTCCACAGCATCTACTGTCTGACTGTGTAGCGTGGACCGCTA 1046
Qy 423 GTAGTGACGCTGTTCCCGTTGGCGGCGCTGTGCACCGCGCACGCGCCGCTGGCGTGGC 482
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1045 CGTGGCGGTGTGCACCCCATCAAGGCGCGACGCTACCGCGGCGCCACCGTGGCCAAGT 986
Qy 483 TGTACGCTCAGCATCTGGGTAGGCTGTGCGGCGGTGTCTGCGCGGTGTCTGCCCTGCA 542
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
985 GGTGAATCTGGCGGTGGTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 926
Qy 543 CGGCTGTCACC-----CGGCGCGGCGCTTACTGAGTGAAGGCTTCCCCAG 590
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
925 GCGCACGCGCGCCCAACAGCGACGGTGGCTGCAACATGTCTATGCCCCAGCCCGC 866
Qy 591 CCGGCGCTGGAGCGCGCTTTCGCACTGTACAACTGTGCGGCTGTACTGCTGCGCGCT 650
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
865 CCAGCGCTGGCTGGTGGGCTTCGTGTGTACACTTCTCATGGGCTTCTGCTGCGCGT 806
Qy 651 GCTGCCACCTGCGCTGCTGAGGCGCATGCTGCGCCACCTTGGGCGGGTTCGCGGTGCG 710
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
805 CCGGCGCATCTGCTTGTCTAGTGTCTCATCATCGCCAAATGCGCATGTTGGGCGCTCAA 746
Qy 711 CCCCC 715
Db 745 GGCCG 741

RESULT 13
US-10-508-892-1

; Sequence 1, Application US/10508892
; Publication No. US20060014218A1
; GENERAL INFORMATION:
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Weingartner, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; FILE REFERENCE: Neuropeptide FF Receptor 1 (NPFF1)
; CURRENT APPLICATION NUMBER: US/10/508,892
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: PCT/EP03/02685
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: EP 02006654.4
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-508-892-1

Query Match      9.1%; Score 108.4; DB 6; Length 1293;
Best Local Similarity 47.4%; Pred. No. 1.6e-08;
Matches 473; Conservative 0; Mismatches 501; Indels 24; Gaps 4;

Qy 144 CTTGCGCGCGTATGCTGTGGCCCTGTGGGGAACCTCGTGTGTCATCTACGTCACTCG 203
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
147 CTATGCGCTCATCTTCTGCTCTGTCATGGTGGGCAACACCTGTGCTGTTTTCATGCT 206
Qy 204 CGGCCAACAGCCGATGGGACCGTGACCACTTCTATACGCCCACTCTGGGCGCACGGA 263
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
207 CAAGAACCGGCACATGATCTGTCAACCAATGTTTCATCTCAACCTGGTGTCACTGA 266
Qy 264 CGTGACCTTCTCTGCTGTGCTGCTCCCTTACCGGCTGTGTACCGCTGCGCGCTG 323
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
267 CTTGCTGGTGGCATCTTCTGTCATGCCCCACACCCCTTGTGGACAACTCATCTAC 326
Qy 324 GGTGCTGGGGAATTCATGTGCAAGTTCTGTCACATCCAGCAGGTCTCGGTGCAAG 383
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
327 GCCCTTCGACAAATGCCACATGCAAGATGAGCGGCTTGGTGCAGGGCATGTCTGT 386
Qy 384 CACGTGTGCCACTCTGACCGCATGAGTGTGACCGCTGTGTAAGTGTGAGTGTTC 443
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
387 TTCGTTTTCACACTGTGTGGCATTTGCTGTGGAAGGTTCCGCTGCATCTGTCAC 446
Qy 444 GCGCG---CCCTGCACCGCGCACGCGCCCTGCGCTGGCTGTGAGCTCAGCATCTG 500
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
447 CCGCGAAGCTGACCTTGGGAAAGCGCTCGTCAACATCGCCGCTCATCTGGGCGCT 506
Qy 501 GGTAGGCTCTGCGCGGTGTCTGCGCGGTGCTGCGCCCTGACCGCTGTCAACCGG 560
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
507 GCTGCTCATGTGTCTCTCGGCGCTCACGCTACCGCTCACCGTGTGAGGAGCACCA 566
Qy 561 GCGGCGCTACTGTAGTGAAGGCTTCCCAGCGCGCCCTGTGAGCGCGCTTTCGCACT 620
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
567 CATGTTGAGCGCGCAACCGCTCTACCTCTCTACTCTGTGTGGAGGCTTGGCCGA 626
Qy 621 CAACCTGCTGCGGTGTACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
627 GAAGGGCATGCGAGGCTTACACCATGTGCTCTTCTGCGACATCTACCTGGGCGCG 686
Qy 681 GCTGCGCACCTGGGCGGGTTCGCC-----GTGCGCGCGCGCGCGCGCGCG 725
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
687 GCGCTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 746
Qy 726 TAGCGCCCTGAGGGGAGGTGTGTGGCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 785
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
747 GGCGCGCGCGCGCGAGGAGGCTGCGGACCGCGCGAGCATCGCGCGCGAGCGCGCG 806
Qy 786 GCGGCTGTGCGCGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 845
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 807 GCACATGCTGGTATGGTGGCGCTGTTCTTACAGTGTCTGGCTGCCGCTCTGGGCGCT 866
Qy 846 CTTGCTGCTGCAGCGCTGGGCGCGGCTCTTGGCACCCACGAGCTAGCGCGCCCTA 905
Db 867 GCTGCTGCTCATGACTACGGGAGCTCAGCGCGCGAGCTGCACCTGGTCAACGCTCTA 926
Qy 906 CGGCTTAAGACTGGGCTCACTGCAATGCTTACAGCAACTCGCGCGCTGAACCGGCTGT 965
Db 927 CGCCTT---CCCTTCGCGCACTGGCTGGCTTCTTCAACAGCAGCGCAACCCCATCAT 983
Qy 966 CTACGCTTCTCTGGGCTCGCACTTCCGACAGGCGCTTCCGCGCGCTGCTGCCGCGC 1025
Db 984 CTACGCTACTTCAACAGAGACTTCCGCGGCTTCCAGGCGCGCTTCC---GGGCGG 1040
Qy 1026 GCG 1085
Db 1041 CCTTGGCG 1100
Qy 1086 GCTGACCGCGCTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1123
Db 1101 TCTGCACAGCGCGGCTCTTCTGCTGGTGGCGCGCGCGCGCGCGCGCGCGCG 1138

RESULT 14

US-10-992-577-7 ;
; Sequence 7, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JFW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1998-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-992-577-7

Query Match 9.1%; Score 108.4; DB 7; Length 1293;
Best Local Similarity 47.4%; Pred. No. 1.6e-08;
Matches 473; Conservative 0; Mismatches 501; Indels 24; Gaps 4;
Qy 144 CTTGCGGCGCTGATGCTGCTGGCGCTGGTGGGAACTGGCTGATCATCTAGTCACTG 203
Db 147 CTATGGCTCATCTTCTGCTGCTGATGGTGGGCAACCCCTGGTCTGTTCATCGTGT 206
Qy 204 CGGCACAAAGCGGATGCGGACCGTGCACCACTTCTACATCGCAACCTGGGCGGCAACG 263
Db 207 CAAGAACCGGACATGATCTGTACCAACATGTTTCACTTCAACCTGGCTGTCACTGA 266
Qy 264 CTTGACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 323
Db 267 CTTGCTGGTGGGCACTTCTGCTGATGCCACCACTTGGGCAACCTCATCACTGGGTG 326
Qy 324 GGTGCTGGCGACTTCATGTGCAAGTTGTTCACTTACATCAGCAGGCTCTGGTGCAGGC 383
Db 327 GCCCTTCGACAAATGCCAATGCAATGAGCGGCTTGGTGCAGGCGCATGTCTGTGTCGCG 386

Qy 384 CACGTGTGCCACTCTGACCGCCATGAGTGTGGACCGCTGTTACGTGACGGTGTTCCTCGGTT 443
Db 387 TTCCGCTTTTACACTGGTGGCCATTTGCTGTGGAAGGTTCCGCTGCATCGTGCACCCCTTT 446
Qy 444 GGGCG---CCCTGCAACCGCGGACCGCGCGCTGGCGTGGTGTGAGCCTCAGCATCTG 500
Db 447 CGCGGAGAAGCTGACCTTGGGAGAGCGCTCGTCAACCATCGCCGTCTATCTGGCGCGCTGC 506
Qy 501 GTTAGGCTCTGCGGCGGTCTGCGCGCGGTGCTCGCCCTGACACCGCTGTCAACCGGGCC 560
Db 507 GCTGCTCATATGTTGCTTCCCTTGCGCGCTCACGTGACCGCTCACCCGTGAGGAGCACCATTT 566
Qy 561 GCGCGCTTACTGCACTGAGGCGCTTCCCGAGCGCGCGCTTGGAGCGCGCTTCCGCACTGTA 620
Db 567 CATGCTGACCGCGCAACCGCTCTACTCTCTACTCTCTGCTGGAGGCTTGGCCGA 626
Qy 621 CAACCTGCTGGCGCTGTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 680
Db 627 GAAAGGCATGCGCAGGCTTACACCACTGTGCTCTTCTCGACATCTACTGCGCGCGCT 686
Qy 681 GCTGCGCCACCTGGGCGCGGTGCGC-----GTGCGCGCGCGCGCGCGCGCGCG 725
Db 687 GCGCTCATATGTTGTTTATGCGCCCGCATCGCGCGCAAGCTCTGCGCAGGCGCGCGCGCC 746
Qy 726 TAGCGCCCTGCAGGGGCGAGGTGCTGGCAGAGCGCGCAGCGCGCTGCGGCGCAAGTCTC 785
Db 747 GCGCGCGCGCGCGAGGCTGCGGACCGCGGAGCATCGCGCGCGCAGCGCGCGTGT 806
Qy 786 GCGGCTGCTGGCGCGCGTGTCTGCTCTTCCGCGCTGCTGGGCGCGCGCTGCTGCTGCT 845
Db 807 GCACATGCTGCTCATGTTGCTGCGCTGTTCTTCAACGCTGCTGCTGCTGCTGCTGCTG 866
Qy 846 CTTGCTGCTGAGGCGCTGGGCGCGCGGCTCTGGCACCCACCGCAGCTAGCGCGCTA 905
Db 867 GCTGCTCATATGCACTACGGGCGAGCTCAGCGCGCGCGAGCTGCACTTGGTCAACGCTA 926
Qy 906 GCGCTTAAGACCTGGGCTCACTGCTGCTTCTACAGCAACTCCGCGCTGAAACCGCTGCT 965
Db 927 CGCCTT---CCCTTTCGGGCACTGGTGGCTTCTTCAACAGCAGCGCGCAACCCCATCAT 983
Qy 966 CTACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1025
Db 984 CTACGCTTACTTCAACAGAGAACTTCCGCGCGGCTTCCAGGCGCGCTTCC---GCGCGG 1040
Qy 1026 GCG 1085
Db 1041 CCTTGGCGCGCGCGCGCTCGGGGAGCCACAAGGAGGCTTACTTCCGAGCGCGCGCGGCT 1100
Qy 1086 GCTGACCGCTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1123
Db 1101 TCTGCACAGGCGGCTTCTGCTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1138

RESULT 15

US-11-136-527-463
; Sequence 463, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 463
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-11-136-527-463

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Query Match      9.0%; Score 107.4; DB 11; Length 1350;
Best Local Similarity 51.6%; Pred. NO. 2.3e-08;
Matches 246; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

Qy 132 CGTGGCGCTCTTCTCGCGCGCTGATGCTGCTGGGCTGTGGGAACTCGCTGGTCAT 191
Db 132 GGTACACCCCACTGCGCGCTGCTTCTGGTGGGCACTCAGGCAACCTGCTCACTAT 191

Qy 192 CTAGGTCACTCGCGCCACAAGCCGATCGGACCGTGACCAACTTCTACATCGCAACCT 251
Db 192 GCTGTGTGTCTCCGCTTCGCGAGCTCGGCACCACTTCTACCTGTCCAGCAT 251

Qy 252 GCGGCCACGAGAGTGACCTTCTCTCTGTGTGGTCCCTTCAAGGCCCTGCTGTACCC 311
Db 252 GGCCTTCTCGGATCTGCTCATCTTCTGTGATGCCGCTGGACCTCGTCCGCTCTGGCA 311

Qy 312 GCTGCCCGCTGGGTGCTGGGCGACTTCTATGTGCAAGTTCTCACTACATCCAGCAGGT 371
Db 312 GTACCGGCCCTGGAACTTCGGGCGACCTGCTCTGCAAACTCTTCCAGTTTGTACGCGAGAG 371

Qy 372 CTCGGTGCAGGCCACGTGTGCCACTCTGACCGCATGAGTGTGGACCGCTGGTACGTGAC 431
Db 372 CTGCACCTACGCCACGGTCTTACCATCACCGCGCTGAGCGTTCGAGCGCTACTTCGCCAT 431

Qy 432 GGTGTTCCGTTGGCGGCCCTTGACCCGCCACCGCCCGCTGGCGCTGGCTGTCAAGCCT 491
Db 432 CTGCTTCCCTCTGCGGGCCAAAGTGGTGGTCACTAAGGGCCGCGTGAAGCTGGTCACTCCT 491

Qy 492 CAGCATCTGGGTAGGCTCTGCGCGGGTGTCTGCGCGGTGTGCGCCCTGACACCGCTGTC 551
Db 492 TGTCACTCTGGGCGCGTGGCTTTCTGACGCGCGGGGCCCATCTTCTGCTGTGGGCGTGA 551

Qy 552 ACCCGGGCGCGCGCTTACTGACGTGAGGCGCTTCCCGACGCGCGCCCTGGAGCGCGC 608
Db 552 GCACGAAACGGCACAGATCCCGGGACACCAACGATGCCCGGCCACCGAGTTCCGC 608
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Search completed: February 15, 2006, 03:34:10
Job time : 337 secs